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TITLE
JOURNAL
REFERENCE
AUTHORS
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JOURNAL
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                           GlyLeuGluGlyPheSerIleAlaPheLeuSerProIlePheLeuThrIleThrProPhe
                                                                                                                                    ATGACCTCGCTGTGGAGAGAAATCCTCTTGGAGTCGCTGCTGGGATGTTTTCTTGGTCT
                                                               CTCTACCATGACCTGGGACCGATGATCTATTACTTTCCTTTGCAAACACTAGAACTCACT
International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- 6 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Seience,
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Direct Submission
Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
Submitted (29-AUG-2000) Sumio Sugano, Institute of Analysis, Human
University of Tokyo, Laboratory of Genome Structure Analysis, Human
Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
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Sugano, S., Suzuki, Y.,
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//db_xref="GI:10437626"
//db_xref="GI:10437626"
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SLIVQAVTWMSGSHLQRYLRIWGFILGQIVLVVLRIWYTSLNPIWSYQMSKVVILTLS
AIATLDRIGTDGDCSK.PEEKKTGEVATGMASR.RNWLLACAAFGSLVFLTHWVTGTASAAGLL
VSRWAVSGHPHPGPDPNFFGGAVLLCLASGLMLPSCLWFRGTGLIWRVTGTASAAGLL
YLHWWAAAVSGCVPAITTASMWPQTLGHLINGGTNPGKTWTIANIFYLLEIFFCAWCT
AFKFVPGGVYARERSDVLLGTMMLIIGLNMLFGPKKNLDLLQTKNSSKVLFRKSEKY
MKLFLWLLVGYGLLGLGLRHKAYERKLGKVAPTKEVSAAIWPFRFGYDNEGWSSLERS
AHLLNETGADFITILESDASKPYMGNNDLTTWNLGEKLGFYTDFGPSTRYHTWGIMALS
RYPIVKSEHHLLPSPEGEIAPAITLTVNISGKLVDFVVTHFGNHEDDLDRKLQAIAVS
KLLKSSSNOVIFLGYITSAPGSRDYLQUTEHGNVKDIDSTDDRWGCEYIMYRGLIRLG
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/clone_lib="COL"
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/db_xref="taxon:9606"
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Primates;
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                                                                          GlyLeuAsnMetLeuPheGlyProLysLysAsnLeuAspLeuLeuLeuGlnThrLysAsn
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                           ValGlyValGlyLeuLeuGlyLeuGlyLeuArgHisLysAlaTyrGluArgLysLeuGly
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           GTTGGTGTGGGATTGTTGGGATTAGGACTACGGCATAAAGCCTATGAGAGAAAACTGGGC
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Command line parameters:

MODEL-frame+_p2n.model -DEV-xlh
-Q-/cgn2_1/USPTO_spool_VS09809638/runat_21102002_153504_1831/app_query.fasta_1.839
-OB-GenEmbl -QFMT-fastap -SUFFIX=ge -MIMMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXIEN=2000000000
-USER=US09809638_eCGN_11_2231_erunat_21102002_153504_1831 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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30: em_htg_inu:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AK025164	RESULT 1
Homo sapiens	Homo sapiens colon cDNA to mRNA, clone_lib:COL clone:COL05748.	oligo capping; fis (full insert sequence).	AK025164.1 GI:10437625)N AK025164	Homo sapiens cDNA: FLJ21511 fis, clone COL05748.	AK025164 2486 bp mRNA linear PRI 29-SEP-2000		

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Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T., Shibahara, T., Tanaka, T. and Nakamura, Y.

Direct Submission

Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)

NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, Construction, Castly Comparison and Technology.
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Shibahara,T., Tanaka,T
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              GlyLeuAsnMetLeuPheGlyProLysLysAsnLeuAspLeuLeuLeuGlnThrLysAsn 380
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                                                                                                   SerSerLysValLeuPheArgLysSerGluLysTyrMetLysLeuPheLeuTrpLeuLeuf
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                                                                                         Mus musculus, Similar to hypothetical protein FLJ21511, MGC:27925 IMAGE:3584006, mRNA, complete cds. BC016523 BC016523.1 GI:16741399 MGC.
Strausberg, R.
Direct Submission
Submitted (31-OCT
                                                                     Mus
                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 2412)
                                                                                 house mouse
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This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not the content of the content of the column of the collowing selection criteria: Similarity but not the column of the collowing selection criteria: Similarity but not the collowing selection criteria:
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Baylor College of Medicine Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk,
A.M., Holloway, M., Telford, B, Hodgson, A., B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
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/product="Similar to hypothetical protein FLJ21511"
/protein_id="AaH16523.1"
/protein_id="AaH16523.1"
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model. 10 month old virgin mouse. Taken by biopsy."
/clone_lib="NCI_CGAP_Mam1"
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Skala, J., Purnelle, B. and Goffeau, A.
Skala, J., Purnelle, B. and Goffeau, A.
The complete sequence of a 10.8 kb segment distal of SUF2 on the right arm of chromosome III from Saccharomyces cerevisiae reveals seven open reading frames including the RVS161, ADP1 and PGK genes Yeast 8 (5), 409-417 (1992)
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Bolle, P.A., Gilliquet, V., Berben, G., Dumont, J. and Hilger, F.
The complete sequence of K3B, a 7.9 kb fragment between PGK1 and
CRY1 on chromosome III, reveals the presence of seven open reading
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              12 (bases 169581 to 171116; 171683 to 172169) Agostoni Carbone, M.L., Panzeri, L., Muzi Falco Plevani, P. and Lucchini, G.
                                                                                               Defoor, E., Debrabandere, R., Keyers, B., Voet, M. and Volckaert, G. Nucleotide sequence of D10B, a BamHI fragment on the small-ring chromosome III of Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oliver, S.G., van der Aart, Q.J., Agostoni-Carbone, M.L., Alberghina, L., Alexandraki, D., Antoine, G., Anwar, R., B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sor, F., Cheret, G., Fabre, F., Faye, G. and Sequence of the HMR region on chromosome
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Benit, P., Chanet, R., F
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Yeast 7 (5), 533-538 (1991)
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Yeast 8 (3),
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Yeast 8 (2), 147-153 (1992)
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sequence of 9.2 kb left of CRY1 on
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                              Muzi Falconi, M.,
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                               Carcano, C.,
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14 (bases 1 to 315338)
Slonimski,P.P. and Brouillet,S.
A data-base of chromosome III of Saccharomyces cerevisiae
Yeast 9 (9), 941-1029 (1993)
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Submitted (14-FEB-1995) MIPS, D-8033 Martinsried, FRG. Data collected by MIPS on behalf of the European Yeast Chromosome III Sequencing project. Update originating from E.J. Louis Revised by [20]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (25-JUN-1993) MIPS, D-8033 Martinsried, FRG. Data collected by MIPS on behalf of the European Yeast Chromosome Sequencing project. Update originating from E.J. Louis revised by [18]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (28-DEC-1992) MIPS, D-8033 Martinsried, FRG. Data collected by MIPS on behalf of the European Yeast Chromosome Sequencing project. Update originating from A. Jimenez replaced by [14] [18] (bases 1 to 316613)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (29-JAN-1996) R. Gromadka, Protein Biosynthesis, Institute of Biochemistry and Biophysics, Pawinskiego 5A, Warsaw, Poland, Electronic Mail Address: robert@psd.ibb.waw.pl revised by [21]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rotein Ycr77p
Frotein Ycr77p
Frotein Ycr77p
From 11 (6), 581-585 (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TA-repeat microsatellites are
following lines present a summary of the altered entities. The resequenced chrIII contig is 316613 bp with GCG-check: 429 GENETIC ENTITIES valid no longer: vCL012w (YCL014w + YCL012w -> YCL014w / C_B1367 + C_C231->C_A1636).
                                                                                                                       The contig sequence which has been released to the file server in 1992 has been subject to a resequencing project, achieved by the joint effort of G. Valles and G. Volckaerts laboratories. The
                                                                                                                                                                                                                       sequences.
On Jul 3, 2001 this sequence version replaced gi:1907116
                                                                                                                                                                                                                                                                                                                                                                                   Submitted (17-JUN-2001) MIPS Yeast Genome Database, GSF Ingolstaedter Landstrasse 1 D-85764 Neuherberg, Germany,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             revised by 19 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      replaced by [13]
17 (bases 1 to 314957)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yeast 11 (6),
95373282
                                                                                                                                                                                                                                                                                                                    Resequencing project, achieved by
                                                                                                                                                                                                                                                                                                                                                        mips-yeast-adm@gsf.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing project
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                                                                                                                                                                                                                                                                                   sequencing project, achieved by the joint effort of G. Volckaerts laboratories. Munich information center for
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753-759 (1993)
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                                                                                                                                                                                                                                                                                         center for protein
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Db 146617 ATTATTGCCATTGGTGCCTATATT--
                                                                                                                                                                                                                                         Db 146674 TTATATCTG----CCGTTCGTTTCTGAAGCCTTCACGCAATATGGTGTACTTTTAGGAGGT 146618
                                                                                                                                                                                                                                                                                                                                                                    Db 146734 TGGTATATGGGAATCTCAGGTTATGAAGCTGCAATATTGGGTTATTTGGGACCCATTTTC 146675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 146794 GGTTTTCTTTTCTGGTCGAACGTTACGTCCCTGTTATGTAGTATTTTGGCATTTCCCGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
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Pred. No.:
146566 TCTGTAGCTGTGGGAACTTCCATTACCGTTGCAACGTTTGTACAAAATCTAAGATATATC 146507
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                               95 ValLeuAlaLeuGlyValSerSerSerLeu----
                                                                                                                                                                                75
                                                                                                                                                                                                                                                                                                        55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 GlyCysValSerTrpSerLeuTyrHisAspLeuGlyProMetIleTyrTyrPheProLeu 34
                                                                                                                                                                                                                                                                                                                                                                                                                          35 GlnThrLeuGluLeuThrGlyLeuGluGlyPheSerIleAlaPheLeuSerProIlePhe
                                                                                                                                                    LeuThrIleThrProPheTrpLysLeuValAsnLysLysTrpMetLeuThrLeuLeuArg 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YCL073c, PEP Y, 4 aa exchanged
YCL068c (C_F190->C_E260), PEP Y, peptide elongated N-terminally by
70 aa YCL065w, PEP Y, 1 aa exchanged
YCL064c, PEP Y, 3 aa exchanged
YCL061c (C_D853->C_F1096), PEP Y, peptide elongated N-terminally by
243 aa YCL051w, PEP Y, 11 aa altered, 6 aa exchanged, 1 aa
additional, 4 aa less at the C-terminus
YCL050c, PEP Y, 1 aa exchanged
YCL042w, PEP Y, 1 aa exchanged
YCL042w, PEP Y, 8 aa altered, 7 aa exchanged, 1 aa additional
YCL042w, PEP Y, 8 aa altered, 7 aa exchanged
YCL042w, PEP Y, 8 aa altered, 7 aa exchanged
YCL036v, PEP Y, 1 aa exchanged
YCL036v, PEP Y, 1 aa exchanged
YCL036v, PEP Y, 1 aa exchanged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YCL028w, PEP Y, 1 aa exchanged YCL027w, PEP Y, 3 aa exchanged YCL026c-a, PEP Y, 8 aa altered, 7 aa exchanged, 1 aa YCL025c (C_F633->C_F595), PEP Y, 7 aa exchanged, the shorter by 38 aa and the last 5 aa are altered LTR deltaCLO5, 1 nt exchange LTR deltaCLO5, 1 nt exchange
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the nt sequence of YCL014w leads to an elongated polypeptide.) This elongated polypeptide encoded by the current YCL014w resembles the Bud3p polypeptide from the EMBL-Entry (Accession:SC175801;ID:U17580, total length 1636 aa) YCL006c, PEP Y, ORF obsolete, is not an ORF in current Chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEW GENETIC ENTITIES:
YCL26-b (C_2125), PEP Y, new orf
ALTERED GENETIC ENTITIES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YCL076w, PEP Y, peptide elongated N-terminally by 51 aa YCL074w, PEP Y, 3 aa exchanged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEP Y, ORF in identical form now C-terminal part of YCR061W-YCR068W-a (YCR068W + YCR068W-a -> YCR068W - C_C429 + C_A145 -> C_A520), PEP Y, ORF in identical form now C-terminal part of YCR068W YCR103c (C_F111, former ORF in region corresponding to coord. 307255-307587(C)) is obsolete, open reading frame is destroyed by single nt exchange resulting in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEP Y, ORF in identical form now C-terminal part of YCL014w. frame shift in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stop codon after 45 aa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.24e-50
760.00
47.20%
30.40%
20.43%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aa exchanged
                                                                                                                       -GTTCAGATGCCA-:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches:
Indels:
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                                                                                                                    ---GAATTAAGGTTGATT 146567
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126
256
140
31
                                                           ----Ile 105
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439	ProThrLysGluValSerAlaAlaIleTrpProPheArgPheGlyTyr	424	Qy
145613	GCTATCACTAACAGCTAGGTTCGTGTA	145672	Db
423	LeuLeuGlyLeuGlyLeuArgHisLysAlaTyrGluArgLysLeuGlyLysValA	404	Qy
145673		145705	рb
403	LeuValGlyV	385	Qy
145706	TGCAAAAACCTTAACATTCAACTGGTGACTATGGGCAAA	145744	DЬ
384	LeuPheGlyProLysLysAsnLeuAspLeuLeuGlnThrLysAsnSerSerLysVal	365	Qy
145745	GAGAAGATTGAGACGGTTCTTGCCTTTTCTTCCACATTTATCATTATTGGTGCTTTAACA	145804	Дb
364	GluArgSerAspValLeuLeuGlyThrMetMetLeuIleIleGlyLeuAsnMet	347	Qy
346 145805	IlePhePheCysAlaTrpCysThrAlaPheLysPheValProGlyGlyValTyrAlaArg:::	327 145852	Db Qy
145853	TCATTCTCCGTTTATATCTTGTCCTTGCCCAT	145888	Db
326	AsnSerGlyThrAsnProGlyLysThrMetThrIleAlaMetIlePheTyrLeuLeuGlu	307	Qy
145889	AAAACATATGGGTTTATGTCCTA	145936	ф
306	. 2	292	Qy
291 145937	AlaGlyLeuLeuTyrLeuHisThrTrpAlaAlaAlaValSerGlyCysValPheAla	273 145984	Db Qy
14	CTTCTCATATCCACTGCTGTACTTTCAGCTAGAAGCATTACACAATGGCCTAAATATATT	146044	DЬ
272	IleTrpTrpValThrGlyThrAlaSerAla	263	Qy
146045	TCTGTGAAGTTTATGGGCAAGCCATTAGTTCCATGTTTGTTG	146086	DЬ
262	GlyLeuMetLeuProSerCysLeuTrpPheArgGlyThrGlyLeu	248	Qy
247 146087	ProAspProAsnProPheGlyGlyAlaValLeuLeuCysLeuAlaSer	232 146146	Оу
146147	ACG	146206	DЬ
231	PheGlyGluValSerLeuValSerArgTrpAlaValSerGlyHisProHisProGly	213	Qγ
146207	ATTGGCAAATTATTTTTGGCTGTTTTTGGCTCGTTGTTATTCGGAATTCATCAGTTA	146266	DЬ
212		193	Qy
146267	AAAAGGAATGCTCAAGCAAAATCTGCTTCGTTG	146299	рb
192	GlyMe:	173	Qy
,146300	GTGCTTACTGTTTATTCGGCATGCTGTCGCCTTATGTTAATTCAATTTCGAAGGG,	146359	Db.
172	ThrLeuSerAlaIleAlaThrLeuAspArgIleGlyThrAspGly	158	Qy
146360		146410	Db
157	<pre>IleTrpSerTyrGlnMetSerAsnLysValIleLeu</pre>	146	ργ
14	FIRE LEGEBOLY OF THE LEGEBOLY	146467	Db 44
1 4 6		ا د د	
125	ValGlnAlaValThrTrpTrpSerGlySerHisLeuGlnArgTyrLeuArgIleTrpGly ACABATGCGAGACTTTTTTTTTTTTTTTTTTTTTTTTTTT	106	P 09

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                           glutathione S transferase; I/LWEQ domain; Kornberg's mediator (SRB) subcomplex; membrane cytoskeleton assembly; microtubule stability; mitochondrial carrier protein; Protein of unknown function domain; RNA polymerase II holoenzyme; scn1; Tf1-type LTR; yeast SLA2; yeast
                                                                                                                                                                       Actin-related protein; cell polarization; coiled-coil; cut9 interacting protein; dna polymerase zeta catalytic subunit; drug sensitivity; DUF51; endocytosis internalization phase; ENTH domain;
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yeast YCR017C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genome is now being continued with funding from The European Commission. Fourteen European sequencing laboratories, including the Sanger Centre, are participating in the project. Protein coding regions (CDS) have been predicted with the help of computer analysis using the Genefinder program in PomBase (an ACEDB database) with additional predictions for the branch-acceptor sites supplied by the program Sp3splice. CAUTION: It is possible that for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (URL, http://www.sanger.ac.uk/Projects/S_pombe/)
During 1995 to 1996 about 66% of S. pombe chromosome 1 was
sequenced by the Sanger Centre. The sequencing of the S. pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           small overlap between neighbouring submissions. Cosmid c688 is overlapped at the 3' end by cosmid c3G9, SPAC3G9, accession number ALO21O46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  number of introns/exons or we may not have chosen the correct splice donor/acceptor sites.
CDS are numbered using the following system eg SPBC25H2.01c. (pombe), B (chromosome 2), c25H2 (cosmid name), .01 (first CDS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces pombe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The length in codons is given for each CDS.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the World Wide Web.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="SPAC688.01"
/note="SPAC688.01, len:425, SIMILARITY:Saccharomyces cerevisiae, YCQ7_YEAST, hypothetical 107.9 kd protein (953 aa), fasta scores: opt: 1034, E():0, (46.5% identified to the cores of the cores o
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                                                                                                                                                                       /translation="SyfmyInHGWCSYLGGLIFTSYVLIYSFASIRISSFYSPAKVWG
GAFLVYILYSLAHVWVVAYEFVPGGPILRERTSYILIFIGWNLAALVPAYSGESKEPN
KADSSVVDIKQSDSSYRRRSFKKSLLTGFCLALMALKFAIQNWPPYDYTPYHPNEKLF
                                                                                                                                                                                                                                                                                    protein involved in sensitivity
/protein_id="CAB90768.1"
/db_xref="GI:7768477"
                           VVSHNGQYESQLDRRLQSTELARIMRESPRPLVFLGYVVSNVGQEPQTILTRDTGMLD
IEPADYDRWCQYIFYRGVKRIGYARLHRSTITDTELQTGKFLVTKDLGRNVRIDKEHV
                                                                                                     TAGIWTIHFGLDNFMYASENRIRDAVRDMELDVFGLLESDTQRLIMGFRDLTQVLAHD
LGMYADYGPGPDKHTWGAALLSKFPIVNSTHHLLPSPQGELAPAIHATLDVYGELIDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in 430 aa)"
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/chromosome="I"
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/strain="972h-"
                                                                                                                                                                                                                                                                                                                                                                                                      /product="hypothetical protein similar
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.5% identity
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                                   CompLementary...
/gene="SPAC688.04c"
/note="SPAC688.04c, len:242, SIMILARITY:Saccharomyces
/note="SPAC688.04c, len:242, SIMILARITY:Saccharomyces
cerevisiae, YIV8 YEAST, Glutathione transferase GTT1, (234
--- facta scores: opt: 274, E():3.5e-11, (27.0% identity
                                                                                                                                                                                                                                                      /note="gtaagt, splice donor complement(3298. .3315)
/gene="spRac688.03c"
/note="ctaatataaatggacaag, scomplement(3375. .3380)
                                                                                                                                                                                                                                                                                                                                                                                                                              complement(2954 . .2976)
/gene="SPAC688.03c"
/note="ctaatacaacattttaaaaatag,
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/note="ttaacactttataag, splice branch and acceptor"
complement(2337. .2342)
/gene="SPAC688.02c"
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/note="ttaacatatag, splice branch and complement(2103. 2108)
/gene="SPAC688.02c"
/gene="SPAC688.02c"
/note="gtgagt, splice donor sequence"
complement(2257. 2271)
                                                                                                                                                 /note="gtatga, splice donor complement(4047. 4775)
/gene="spac688.04c"
complement(4047. 4775)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MICWPSLIKESWNDKEYCYYCFEVVAATLEHRKVRDKWNAKSWT 
/SIPLFVKFASGKGHDKQLRGCIGTFRARJUNLTYFSAACDERFRPISLGELA 
LLECQIDLLVDFEPIDDPLDWEVGHGVSIKTTANGIRYSSTYLPSVAAEQRWDQEET 
LESLIHKAGYYGSIRSLQITATRYKSLEIGCTYEEYLHNLELLG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="gtgtgt, splice donor sequence" complement(join(2596. .2953,3083. .3297,3381./gene="SPAC688.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(1545. .1979,2109. .2256,2343.
/gene="SPAC688.02c"
complement(join(1545. .1979,2109. .2256,2343.
                                                                                                                                                                                                                                                                                                                                                                                          complement(3077.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Match to PF01871 DUF51, Score 49.41"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(2662. .2953,3083. .3273))
/gene="SPAC688.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="conserved hypothetical protein"
/protein_id="CAB90770.1"
/db_xref="GI:7768479"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9Y4X0, ammecr1 protein., (333 aa), fasta scores: opt: 443, E():3.4e-25, (40.3% identity in 186 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QDKEVENPDEQTSTTVFRKEDIDRYEQTIAKVAYLKKNLPRVVARLEKTP
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SREAGMGREDQLRIRVKEMLMELIESTFSIIQENVTINGFDANSALQDPKNSDQIEPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cerevisiae, Q12143, chromosome xvi reading frame orf yp1233w., (216 aa), fasta scores: opt: 183, E():9.1e-05 (22.7% identity in 185 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                              acceptor'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="SPAC688.03c"
/note="SPAC688.03c, len:204, SIMILARITY:Homo sapiens,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="hypothetical protein with very low similarity to yeast ypl233w"
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/note="SPAC688.02c, len:210, SIMILARITY:Saccharomyces
/label=SPAC688.04c
                                                                                                                                                                                                                                  /gene="SPAC688.03c"
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                                                                                                                                                                                                                             CysalaTrpCysThralaPheLysPheValProGlyGlyValTyrAlaArgGluArgSer 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTAATTTACTCGTTCGCTTCTATC--
                                                                                 AspValLeuLeuGlyThrMetMetLeuIleIleGlyLeuAsnMetLeuPhe-----
                                                                                                                                                                                 ATGTATATTAACCATGGATGGTGAGTTATTTGGGTGGGTTAATATTTACTTCCTACGTT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="ttaactgagctttag, complement(6921. .6926)
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/gene="SPAC688.06c"
/complement(join(5637. .6842,6927. .6980))
/gene="SPAC688.06c"
/note="SPAC688.06c, len:419, predicted to contain force coiled-coil region, SIMILARITY:S. cerevisiae, LOW to
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SIDSTCQSNSFLEGDSATHKKKKTDNIKEFTSCEFNDRSRTLLNYAGYMDTNKNADNE
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FAGEQFTAADPQMCFPTFAAQRDYLSQKPYKNTKRWMRVVSDRPACRTAÄEKVEDNTL
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/protein_id="CAB90771.1"
/db_xref="GI:7768480"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SPAC688.06c"
/note="qtatco
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Submitted (15-NOV-1996) Sachiyo Yoshioka, Tsukita Cell A
Submitted (15-NOV-1996) Sachiyo Yoshioka, Tsukita Cell A
ERATO JST, Kyoto Research Park; 17 Chudouji Minamimachi,
Shimokyo-ku, Kyoto, Kyoto 600, Japan
(E-mail:syoshi@cell.tsukita.jst.go.jp, Tel:+81-75-315-79
Fax:+81-75-315-6420)
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/db_xref="G1:1749468"
/translation="Itspasirizessyspakvwggaflvyilyslahvwvaxefvpg
/translation="Itspasirizessyspakvwggaflvyilyslahvwvaxefvpg
GPILRERTSYILIFIGWNLAALVPAYSGESKEPNKADSSVVDIKOSDSSYRRSFKKS
LLTGFCLAEMALKFAIOMMPYDYTPYHPNEKLFTAGTWTIFFGLDNFWYASENRIRD
AVRDELDVFGLLESSTORLIWGFDLTQVLABLDLGWYADSGPGDKHWGAALLSKF
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/clone="SY 0503"
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/strain="PR745"
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This STS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces Servazzii, Zygosaccharomyces rouxii, Saccharomyces Servazzii, Zygosaccharomyces rouxii, 12 Saccharomyces Servazzii, Saccharomyces Servazzii, Zygosaccharomyces 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic Exploration of the Hemiascomycetous Yeasts: 1. A set yeast species for molecular evolution studies(1) FEBS Lett. 487 (1), 3-12 (2000)
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Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
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Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                      ATTGACCCTACTGACGATGATAGGTGGTGTGA-TATATCTTGTATAAAGATTTGAGAAGA
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Direct Submission

Submitted (07-NOV-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6: On Jul 3, 2001 this sequence version replaced gi:12057004.
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Submitted (05-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
                                                                                                                                                                                                                                                               Waterston, R.H.
Direct Submission
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Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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                                                                                                                                                                                                                             Submitted (03-JUL-2001) Genome Sequencing Center, Washin University School of Medicine, 4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                Waterston, R.H.
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Contact: sapiens@watson.wustl.edu
----- Summary Statistics
Center project name: H_NH0317G22
                                                   Web site: http://genome.wustl.edu/gsc
                                                                Center: Washington University Genome Center code: WUGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                 BAC clone
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Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                 RP11-317G22
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complete
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Parkway, St.
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                                                                                                                                   63108,
                                                                                                                                                                                                                                                                                                                                Louis,
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                                                                                                                                   USA
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

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B 8

40 40 The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome

FEATURES

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The clone sequenced to the left is AC011956. Actual start of this clone is at base position 1 of RP11-317G22; actual end is at base position 184206 of RP11-317G22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence fidelity of RP11-317G22 between bases 17725 to 17956
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                                                                                                                                                                                                                                                                                                                                      Insert size: 219685; sum-of-contigs
Insert size: 126549; 14.0% error; agarose-fp
Quality coverage: 3.63x in Q20 bases; sum-of-contigs Quality
coverage: 6.72x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CBIO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requestes clonerequest@sanger.ac.uk
On Aug 29, 2000 this sequence version replaced gi:9926474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 222885)
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                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
3599: contig of 3599 bp in le
3600 3699: gap of 100 bp
3700 12818: contig of 9119 bp in le
12819 12918: gap of 100 bp
12819 16398: contig of 3480 bp in le
16499 18590: contig of 2092 bp in le
18591 18690: gap of 100 bp
18591 18690: gap of 100 bp
22373 22472: gap of 100 bp
22473 26905: contig of 4433 bp in le
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82666 82765: gap of 100 bp
82766 87239: contig of 4474 bp in length
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3700. .12818
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12919, .16398
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/chromosome="6"
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135261: contig of 3383 bp
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107564: contig of 4048
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222885: contig of
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197829: contig of 4258
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97550: contig of 3779 bp in length
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65124: contig of 9425 bp in length
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99: contig of 6963 bp in length
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93772, .97550
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82766. .87239
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29682, .33446
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197930. .222885
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169051. .17372
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131879. .135261
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Homo sapiens chromosome 6 clone Rt
PROGRESS ***, 33 unordered pieces.
AL158816
                                                                                                                                                                                                                                                                                                                                                                       Insert size: 219685; sum-of-contigs
Insert size: 126549; 14.0% error; agarose-fp
Quality coverage: 3.63x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                    Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; LO8752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 204390 bases at least Q40 Consensus quality: 211527 bases at least Q30 Consensus quality: 215491 bases at least Q20 Consensus quality: 215491 bases at least Q20
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Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requestes: clonerequest@sanger.ac.uk
On Aug 29, 2000 this sequence version replaced gi:9926474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: dJ405B4
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1 (bases 1 to 222885)
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HTG; HTGS_PHASE1;
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                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                  be preserved.
301 3599: contig of 3599 bp in length 3700 12818: contig of 9119 bp in length 12819 12918: gap of 100 bp 162919 16398: contig of 3480 bp in length 16399 16498: gap of 100 bp 16499 18590: contig of 2092 bp in length 16499 18590: contig of 2092 bp in length
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ASE1; HTGS_CANCELLED
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141050 156466: contig of 15417 bp in length
156467 156566: gap of 100 bp
156567 164836: contig of 8270 bp in length
164837 164936: gap of 100 bp
164937 168950: contig of 4014 bp in length
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16499. .18590
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/db_xref="taxon:9606"
/chromosome="6"
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0 222885: contig of 24956
Location/Qualifiers
/note="assembly_fragment:00125"
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/clone_lib="RPCI-3"
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22473. .26905
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                                                                                             in codons is given for each CDS.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid c589 is overlapped at the 5' end by cosmid c16A10, EMBL entry SpAc16A10, accession number Z97185, and at the 3' end by cosmid c688, EMBL
                                                                                                                                                                                                                                                                                                        number of introns/exons or we may not have chosen the correct splice donor/acceptor sites. CDS are numbered using the following system eg SPBC25H2.01c. SP (5. pombe), B (chromosome 2), c25H2 (cosmid name), .01 (first CDS), c (complementary strand). The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Commission. Fourteen European sequencing laboratories, including the Sanger Centre, are participating in the project. Protein coding regions (CDS) have been predicted with the help of computer analysis using the Genefinder program in PomBase (an ACEDB database) with additional predictions for the branch-acceptor sites supplied by the program Sp3splice. CAUTION: It is possible that for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             i norganic phosphate transporter; metaxin 2; mitochondrial outer membrane protein; phosphatidylinositol metablolism; spindle integrity WD domain; ubiquitin-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (01-JAN-2001) European Schizosaccharomyces genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 1SA, E-mail: barrell@sanger.ac.uk and Katholieke Universiteit Leuven, Laboratory of Gene Technology,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S.pombe chromosome I cosmid AL512496
                                                                       entry SPAC688, accession number AL355632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (URL, http://www.sanger.ac.uk/Projects/S_pombe/)
During 1995 to 1996 about 66% of S. pombe chromosome 1 was
sequenced by the Sanger Centre. The sequencing of the S. pombe
genome is now being continued with funding from The European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wood, V., Rajandream, M.A., Barrell, B.G., Aert, R., Robben, J., Weltjens, I., Grymonprez, B. and Volckaert, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Details of yeast sequencing at the Sanger Centre are available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kardinaal Mercierlaan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fission yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL512496.1 GI:12043544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 individual CDS we may have underestimated or overestimated the
                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 to 18342)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ascomycota; Schizosaccharomycetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 bp
c589.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLN 04-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        513
         misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
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                                                                                                                                                                                                                                                                                                                                                                                                                               TSISOSNTSPNLNTHENIPKOMEIQSDRMVTEDLNPYNVEVDIPEISÄNISDSKIPT
SAYMPSYYSAVIFPSSISSIFOKYNYGGKYWCPSPSLSTEDLFESFSVABSVTSTDED
ICSTNETQODETMEYNHDFESSSKTPTNISEOSNPDSNYDTLSLAHOYLMUESKSANF
EFSELKSLDLQPTITLGKNDLLNAILSONLMFRSLPFWKSMTTSFMMSÖDVLNFSSYM
KKPIRDYLEKILLGESSAVELSKSPENYLSSINNGHHALNDNPSGVNRSETLNFSSYM
PRVLLKYNEKKLSLDSSAPENNISLCLQPYGESKDFEVFLLSSKSPDYSKAISFT
PVGLAYENCKLGKLNLSETSINERYMGFSTNINETDNYDDNETTOSDTATSYEQLASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LCKEYNFVPIYGVLLPLKLHPSFDTQLWNIYGYPVVDLQLSVLSKGHIËFYLKPTRQT
VYRLSEVDNLVKKLDTVIRLAPTGCLAFITSVHANASAQTVDALKHRYGFSLTTTSKW
VGYTLESSALEFSWFLELGFLETSALRMNDDSLSSNLTDLNILVLPSNVVNNKKELTE
FANEBAEASDKKKEGFTEKEETADAVVTLVPSHSSSPVRYSINSAKSTĖASIKVNEEI
LVADHNVSDDILMEEIDDVGITEADFDYFDLPNVEEKVEMIEPNFANTÄTTLDNEEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="gtacgt, splice donor sequence"
complement(join(967. .4482,4518. .466
/gene="SPAC589.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="ctgaccaagcgaatag, splice branch and
complement(115..120)
/gene="SPAC589.01c"
                                                                                                                                                                                                                                                                                                                                                                          CVNELSGKNVLFFYFLEDDSEKLLKACQHFICVKDSIKRLGDNKFEDKŞLRICTIPNSIFDSPNSHTTNSNSFFTKVSLDIYNNDPLLMDGSLKRREPAFLLKKPLLSTLNYQLKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="msvCfkKyvKmRQWPHVLSLRvYASYFLLYNNLPESSAMVHDGV
HLISIKTILTDQPCPNTIYYAKYQVQRKDNEDAASLLEDKEAYLRNQDÇIVHAKNDLL
FVYDFQAIPSIPEESSSFMLLNSGAFSRLALFQKDELALLLDLYINFLQGLKKTVLYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(967. .4482,4518.
/gene="SPAC589.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SILCKQLKELDLVVSSNKEFLNEKTSDQISFLKPRETVVEKKLANGSIWPNETSHLDK
SRDLSSHSNGLDALAMTPYIVKENNKTHLSPRGNYPSEAEKSCDFYGQPLHFYRENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     scores: opt: 111,
                                                                                                                                                                                                                                                      DEDESYLPLLSIHLLISRNHDPYLMLNLILKHYLSMIYLQFRTYVSFSSLPLHISTVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical
/protein_id="CAC19759.]
/db_xref="GI:12043546"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="SPAC589.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="hypothetical protein"
/protein_id="CAC19758.1"
/db_xref="GI:12043545"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(1. .65,121.
/gene="SPAC589.01c"
                                                                                                                                                                                                                       YQKQLLQFMASDITHPVTS"
                                                                                                                                                                                                                                                                                                                  VTFTFLNSMHMDWIVIVMKIGEMSDAEYLFWDQAIIPENLQGNVSLTVĞYCSAEHGPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KDSNQIQELENLLRKEKQRNTE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCLYGSSLSNVFTEKSSDYRHGLGSPTSLVSSNTASKLHLGRKDIVKLSELRNCINSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/label=SPAC589.01c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(1. .65,121. .777))
                                                                                                                            /note="ataacatgataaattaaaag,
                                                                                                                                                            /gene="SPAC589.02c"
                                                                                                                                                                                                                                                                                                                                              INPRSSALGEYALHVTYTTVEEHLLICNWNDSYGEFETERRYFLQDLEJEDALQQILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/label=SPAC589.02c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="SPAC589.02c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="SPAC16A10.08c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SPAC589.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organisme"Schizosaccharomyces
/strain="972h-"
/db_xrefe"taxon:4896"
/chromosome="I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MKKHKSSIKCFKIDQISQQPETDLVFTKRSECKVKDELFSDKEN/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="SPAC589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SPAC589.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /partia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="nominal overlap with SPAC16A10 S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q21148,
                                     splice donor sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .01c, very low SIMILARITY:Caenorhabditis
18, k02f3.4 protein., (308 aa), fasta
11, E():2.4, (23.3% identity in 193 aa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             len:1224"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ıı protein"
                                                                                                                            splice branch and acceptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4667,4770.
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acceptór"

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gene
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                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mitochondrial outer membrane protein putative component of a preprotein import complex"
/protein_id="Cacl9761.1"
/db_xref="cd::12043548"
/translation="MGGLTKFSSYFHSIFSRFPLITFSNPYPGENEDYKTKTVMYLTM
/WRSDLMSEALDVNSLOWGTWAKLNDPSIVFLNVSNHASPDEKVPFIQIESRKLYLNPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(5999. 6559,6639. 6893)
/gene="SPAC589.04"
/note="SPAC589.04"
/note="SPAC589.04, len:272, SIMILARITY:Homo
075431, metaxin 2., (263 aa), fasta scores:
E():2.le-07, (29.2% identity in 216 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="hypothetical protein"
/protein_id="CAC19760.1"
/db_xref="GI:12043547"
/db_xref="GI:12043547"
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/translation="MDLSLFSDIKDVVERDMKKNSKVVENSSARSLKNKTEENKTIDK
/translation="MDLSLFSDIKDVERDMKKNSKVVENSSARSLKNKTEENKTIDK
/translation="MDLSLFSKNSVGLLHDIKELGGTEEDLELIEDVESDEELEFE
HKSSVGPKEDGTDAFANELNLFAKKLGFSKNSFDARALDTESEDETEIEKSSSENSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAC19762.1"
/db_xref="GI:12043549"
/db_xref="GI:12043549"
/translation="MSRVLQDAEFISLNSNDVKVNKGGCAAVATWIKEKLDSLGPOFA
EWQNHELHPKTRDVSTLDWIFLYDILNFSFWSDYDVEDSGKHSKRFSIEYKGKLYTGY
WSLCAAINKALDAGIPITSPAFYADEKQCPDTLIASVFDSATVEKIPLLEERIRIMRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="ctaatatcctctgttttag,
complement(5369. .5374)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="SPAC589.02c"
/note="gtatat, splice donor sequence"
complement(join(5153. .5311,5375. .577
/gene="SPAC589.03c"
             SGRVLVDSYHGSYCGLLKKCHNQAQRLIKLLLADFPDFRDVSVYKGRECYMLKRAQIL
VAETWACFQGQNYGRFDDIDSITMFADYRVPQILWQLGCLSYSSDFKKRLLKNELIAH
                                                                                                                               glycoprotein
                                                                                                                                                                                                                                                                                                             /note="ctaacaaagcttag, complement(join(7189.
                                                                                                                                                                                                                                                                                                                                                                                                                                               LLQYFLKDESTLQQISPWMSLLINQVETAILLTMYLDNENFSEIQKKWLPNMSWPLNI
IKSIGLPSQIKRKICLQLNESTLDFDAILEDASKAFSALSELLGSDKWFFNNESPSFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(5312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(4764.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="SPAC589.02c"
/note="ttaacagtaaaagtatcag, splice branch
                                                                                                                                                                                                                                 crassa.,
                                                                                                                                                                                                                                                                              complement(join(7189. .8041,8175.
                                                                                                                                                                                                                                                                                                                                                                                                                                 DVSLFAHAEIINHLPLKNDQLKVVLGTHKNLTDLTTRVRTLAGYTSAGPIALR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="gtaagt, splice donor s
join(5999. .6559,6639. .6893)
/gene="spac589.04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VDVDSDDE"
 NDPME I EMRGC S I WAVEK I LQN I NRKDVNA I T I DFFLWDLAK EWQAKGYKPSTQVDEV
                                                                                                                                                                                                                              /gene="SPAC589.05c"
/note="SPAC589.05c, len:347,
crassa., CAB98246, conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="SPAC589.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="SPAC589.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label=SPAC589.03c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                               /product="conserved
                                                                                                                                                                /label=SPAC589.05c
                                                                                                                                                                                                                                                                                               /gene="SPAC589.05c"
                                                                                                                                                                                                                                                                                                                                                /gene="SPAC589.04"
                                                                                                                                                                                                                                                                                                                                                                               /note="gtacgt, splice
                                                                                                                                                                                                                                                                                                                                                                                                /gene="SPAC589.04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="mammalian metaxin 2 homologuue; putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label=SPAC589.04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 aa)"
                                                                                                                                                                                                              fasta scores: opt:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .4769)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .5330)
                                                                                                                                                                                                                                conserved
                                                                                                                                               hypothetical
                                                                                                                                                                                                                                                                                                            , splice branch and acceptor" .8041,8175. .8323,8370. .840
                                                                                                                                                                                                                                                                                                                                                                                 donor
                                                                                                                                                                                                              997,
                                                                                                                                                                                                                                                                                                                                                                               sequence'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 splice
                                                                                                                                                                                                             SIMILARITY: Neurospora hypothetical protein., (3: E():0, (46.3% identity in
                                                                                                                                               protein;
                                                                                                                                                                                                                                                                                .8323,8370.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .5722))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  branch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
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                                                                                                                                             putative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acceptor"
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                                                          TTTATATCAATCAGGTGCTTTTATGCTTATTGGATTTGTTTTTAGCCTGCTTCGGATCATA 17919
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               Peery, J., Perez, L., Peters, L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (12-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 68 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: Estimated insert size may differ from sequence length
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----- Summary Statistics
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Contact: hgsc-help@bcm.tmc.edu
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (06-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqrefégenoscope.cns.fr - Web : www.genoscope.cns.fr)
This STS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
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Bolotin-Fukuhara, M., Bon, B., Brottier, P., Casaregola, S.,
de-Montigny, J., Dulyon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincher, B. and Wolffer, B.
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Wincker, P., Artiguenave, F. and Souciet, J.
Genomic Exploration of the Hemiascomycetous Yeasts:
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Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
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Saccharomycetales; Saccharomycetaceae; Zygosaccharomyces.
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T3 end of clone AR0AA022A01 of library AR0AA from strain CBS 732 of
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FEBS Lett. 487 (1), 52-55 (2000)
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                                                                                                                                                                                                                                                                                                                      GGGTTACCTTATATCTTGGGTGTGATTTGGACCATTCCATCATATTTTGCAGCTTTGAGT 703
                                                                                                                                                                                                                                                                                                                                                                                      GAATCTACTTGGGTCTTGTGCAATAGAAACATTACTGAATGGGATAACTATCTTTACGGT 643
                                                                                                                                        PheValProGlyGlyValTyrAlaArgGluArgSerAspValLeuLeu 353
                                                                                                                                                                                                                                                     GAATTACAGAGTGTTGGCGTCATAATT ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAAATACA - - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ArgTrpAlaValSerGly-----HisProHisProGlyProAspProAsnProPheGly 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AlaPheGlySerLeuValPheLeuThrHisTrpValPheGlyGluValSerLeuValSer 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValThrTrpTrpSerGlySerHisLeuGlnArgTyrLeuArgIleTrpGlyPheIleLeu [128
                                                                                                                                                                                   CTAGGTTTTGTTACCTATGCGTTCATCAGTTTTGCCACTGTTTGGACCGTTGCGTATGCA 790
                                                                                                                                                                                                                 IleAlaMetIlePheTyrLeuLeuGluIlePhePheCysAlaTrpCysThrAlaPheLys 337
                                                                                                                                                                                                                                                                                 TrpProGlnThrLeuGlyHisLeuIleAsnSerGlyThrAsnProGlyLysThrMetThr 317
                                                                                                                                                                                                                                                                                                                                                                                                           LeuHisThrTrpAlaAlaAla-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ArgGlyThrGlyLeuIleTrpTrpValThrGlyThrAlaSerAlaAlaGlyLeuLeuTyr 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGG-----TTAACTTGCCTTGTCATGCTATTAGCTTCTTTAACCTCCGTGAGATTCTCT 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATTGGTCTTGGGAGGGTTGGAACCAAGAAACTCAAGGCCCCTTGGCTTGGCCATGGAGT 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGATTCGGTTCCATAATTTTTAGTCTTCACCGATTCTTTACCGATGCCTCTGCATTGATT 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAATCTTGGCA----CCTTATGTCAATTCATTACATTTTGCTCCCAAAGATAGTTCTAAG '316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AlaIleAlaThrLeuAspArgIleGlyThrAspGlyAspCysSerLysProGluGluLys 180
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                                                                                                                   TTTGTTCCTCTTGGATGGTTATTGAGAGAAGAATCGAGGTTGTATTTG
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          225532 bp DNA linear
Rattus norvegicus chromosome Rf1 clone CH230-59C15,
SEQUENCE, 20 unordered pieces
AC096364
                                                                                                                                                                                                                                                                                                                                                    -ValSerGlyCysValPheAlaIle-----PheThrAlaSerMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----TGGGTACCTGGTATC--
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                                  HTG 20-D
WORKING
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REFERENCE
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Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,
Martinez,E., Massey,E., Mawhiney,E., Mitchell,T., Mohabbat,K.,
Morgan,M., Morris,S., Moser,M., Nickerson,E., Nwokenkwo,S.,
Nguyen,A., Nguyen,N., Nickerson,E., Nwokenkwo,S.,
Nguyen,A., Nguyen,N., Nickerson,E., Nwokenkwo,S.,
Nguyen,A., Nguyen,N., Pickens,R., Pace,A., Payton,B.,
Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M.,
Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N.,
Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,
Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,
Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N.,
Thomas,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S.,
Warlington,S., Ward-Moore,S., Warren,R., Washington,C.,
Watlington,S., Wallams,G., Williamson,A., Wleczyk,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Nivort Schwisterson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carter, M., Cavazos, S.R., Chacko, J., Chaveland, C.D., Cox, C., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Cyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Cyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunararne, P., Hale, S. Hamilton, K., Harris, C., Harris, K., Hart, M., Haylak, P., Hawes, A., Hamilton, K., Harris, C., Hodgson, A., Hogues, M., Holloway, C., Holloway, C., Holloway, C., Harris, K., Hart, M., Haylak, P., Hawes, A., Holloway, C., Harris, C., Harris, C., Hodgson, A., Hogues, M., Holloway, C., Holloway, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Benton,J., Bimage,K., Blankenburg,K., Bunnau,C.,
Benton,J., Bimage,K., Blankenburg,K., Bunnau,R.P., Buhay,C.,
Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Chen,G., Chen,R.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Muzny,D.M., Adams,C., Adio-Oduola,B., All Ushkari, ..... Barbaria,J., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Renton.J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Routh, B., Buhay,C.,
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On Dec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (17-SEP-2001) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 225532)
Consensus quality: 220440 bases at least Q40
Consensus quality: 221708 bases at least Q30
Consensus quality: 222752 bases at least Q30
Constituence insert size: 216271; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 10.2x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: GEZQ
Center clone name: CH230-59C15
----- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                            Assembly program: Phrap; version 0.990329First call
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           norvegicus
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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US-09-809-638-2 (1-699) x AC096364 (1-225532)
                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                       BASE COUNT
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                                                               Query Match:
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                                                                                                 Score:
                                                                                                              Pred.
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_da
NOTE: This is a 'working draft' sequence. It currently
consists of 20 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as soon as it is available and the accession number will
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                                                                                                                                                                   /clone="CH230-59C15"
                                                                                                                                                                            /chromosome="Rf1"
                                                                                                                                                                                         /db_xref="taxon:10116"
                                                                                                                                                                                                    /organism="Rattus
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214157 GTCCACACATCTTTACTT-----GCAATGAGTCATTGGTCTGGTTCGAGGTCTCTGGCT 214104

긎 ,	214103		314044
Qγ	131		150
뮹	214043	TGTGTTATGGAGGTCCTACAGCTTTGGATCTGCAGGACCTGCCCCTTCATGAGCTCCAGC	213984
Qy dd	151 213983	WetSerAsnLysVallleLeuThrLeuSerAlaIleAlaThrLeuAspArgIleGlyThr	170 213927
B &	171 213926	AspGlyAsp	185 213867
子 &	186	AlaThrGlyMetAlaSerArgProAsnTrpLeuLeuAlaGlyAlaAlaPheGlySer ::: ::: :::	204
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₩ Ş	205	LeuValPheLeuThrHisTrpValPheGlyGluValSerLeuValSerArg-Tr	222 213783
B 84	222	pAlaValSerGlyHisProHisProGlyProAspProAspProPheGlyGlyAlaValLe	242 213724
₽ 8	242 213723	uLeuCysLeuAlaSerGlyLeuMetLeuProSerCysLeuTrpPheArgGl	259 213664
₽ &	259 213663	YThr61yLeuIleTrpTrpValThrGlyThrAlaSerAlaAlaGlyLeuLe	276 213604
요 성	276 213603	uTyrLeuHisThrTrpAlaAlaAlaAlaValSerGlyCysValPheAlaIlePheThrAlaSe: :	296 213559
p Q	296 213558	<pre>IMETTIPPTO-GlnThrLeuGlyHisLeuI :</pre>	306 213499
B 8	306 213498	leAsnSerGlyThrAsnProGlyLysThrMetThrIleAlaMetIlePheTyrLeuLeuG	326 213473
₹ Ş	326 13472	LuIlePhePheCysAla	331 213418
용 성	332 213417	CTCTCCCCATGTTCCCCAGGCAAGGGGTGAAGCCAGTTCTGCACAGCCCTCAAAAGTCAAC	340 213358
₽ 2	340 21335 <i>7</i>	roGlyGlyValTyrAlaArgGluArgSeraspValLeuLeuGlyThrMetM:	357 213298
β Σ	35/7 21329/7	etLeuIleIleGlyLeuAsnMetLeuPheGlyProLysLysAsnLeuAspLeuLeuG::: ::: 	377 213251
β Σ	377 213250	In	387 213191
3 5	387	rgLysSerGluLysTyr	397
Ş	ω S	TrpLeuLeuValGlyValGlyLeuGlyLeuGlyLeu	10

	0.0351 (bases 1 to 31717) ger,K.J. and Harris,D.	JO ME REFE AU
al map	Kinashi, H. and Hopwood, D.A. A set of ordered cosmids and a detailed genetic and ph for the 8 Mb Streptomyces coelicolor A3(2) chromosome	TI
n,J.,	lhobacteria, Acthobacteridae; nycineae; Streptomycetaceae; Strep , Denapaite,D., Eichner,A., Cullu	REFE
odon.	regulator multi-domain beta keto-acyl synthase; TTA Leu c Streptomyces coelicolor A3(2). NISM Streptomyces coelicolor A3(2)	SOURCE ORGA
2.	ALIO9747.1 GI:5708233 ALIO9747.1 GI:5708233 ABC transport system ATP-binding protein; bldA codon;	VERS
-AUG-199	LT 15 1/c S NITION	RESUL SCJ21 LOCUS DEFIN
	590 pTyrLeuGlnLeuThrGluHisGlyAsnValLysAspIleAspSerThr 606 :::::: ::: ::::: ::: 112484 GTTTGTGATTCTCTCCAGGAAGCAGAACTCCATACAGGATGTGCCTGTCACT 212433	Qy Db 2
590 212485	574 nGlnValllePheLeuGlyTyrIleThrSerAlaProGlySerArgAs ::: ::: ::: ::: :12540TAAGTCCCCCTTGGTCATTCCCAGATTCCCTTATTCTGATCCCCAGGTTCAGAAG	Qy Db 2
574 212541	558 gLysLeuGlnAla	Qy Db 2
558 212587	539 GlyLysLeuValAspPheValValThrHisPheGlyAsnHisGluAspAsp-LeuAspAr	Qy Db 2
538 212647	519 LeuLeuProSerProGluGlyGluIleAlaProAlaIleThrLeuThrValAsnIleSer	Qy Db 2
518 212706	504 IleMetAlaLeuSerArgTyrProIleValLysSerGluHisHis ::::	Qy Db 2
503 212766	485 GluLysLeuGlyPheTyrThrAspPheGlyProSerThrArgTyrHisThrTrpGly	Qy Db 2
484 212805	466 GluSes ::: 12863 GACTCC	Оу Db 2
465 212864	447 LeuGluArgSerAlaHisLeuLeuAsnGluThrGlyAlaAspPheIleThrIleLeu 	Qу Дъ 2
446 212924	427 luValSerAlaAlaIleTrp-ProPheArgPheGlyTyrAspAsnGluGlyTrpSerSer	Qy Db 2
427 212952	416	Qy Db 2
415 213011	411ArgHisLysAlaTyr	Db 2
213071		pb 2

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parkhill, J., Barrell, B.G. and Rajandream, M.A.

Direct Submission
Submitted (03-AUG-1999) Streptomyces coelicolor sequencing project,
Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for small overlap between neighbouring submissions.

Cosmid J21 lies between J11 and J33 on the AseI-J genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces coelicolor sequencing at The Sanger Centre is fi
by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are
available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   strand).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             upstream initiation codon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nttp://www.nih.go.jp/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L; http://www.sanger.ac.uk/Projects/S_coelicolor/)
are numbered using the following system eg SC7B7.01c. SC (S.
licolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       also included but some of these may be fortuitous. length in codons is given for each CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           more significant matches with motifs in the PROSITE database
/note-"SCJ21.02c, probable ABC transport system ATP-binding protein, len: 204 aa; similar to many e.g. NUC_ECOLI high-affinity zinc uptake system ATP-binding protein (251 aa), fasta scores; opt: 327 z-score: 404.3 E(): 3.6e-15, 35.2% identity in 179 aa overlap. Contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="cosmid J21"
complement(1. .342)
/gene="SCJ21.01c"
                                                                                                                                                                        complement(339. .953)
/gene="SCJ21.02c"
                                                                                                                                                                                                            /gene="SCJ21.02c"
complement/330
                                                                                                                                                                                                                                                                                                                    PDQPAPERLRATGEVLSPPGNHLTQITGALNAVTLIAGFMMFAATFTGGAFDRRLAMA
GYPRFHLVLAKL"
                                                                                                                                                                                                                                                                                                                                                                                 /product="putative integral membrane protein"
/protein_id="CAB52347.1"
/db_xref="G1:5708234"
/translation="MRRHLSLFVTASRYALIGHARNRFAMLLVVVYIPVWIALAYVTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="SCJ21.01c, probable integral membrane
partial CDS, len: >114 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(<1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="nominal overlap with StJ11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Streptomyces
/strain="A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="SCJ21.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:100226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coelicolor sequencing at The Sanger Centre is funded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .342)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coelicolor A3(2)"
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CDS

AAAMTFRAMLGDGEPSARPLPGGSGVFGVPRRFGAAVALATRFLARTFTVRRHRPDPA HVYEVVADGPADWDTALHSALNAPFAPGAYWGVWLIHGHEPDAYALCYRFLHACQDGS EVRWDAGGVAYLSGPPPSLADLRAYVAFRLGELPLLTSRVTGGRRPGWQPSEDFPVDR

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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               forming) (532 aa), fasta scores; opt: 938 z-score: 1016.9 E(): 0, 38.7% identity in 432 aa overlap. Also similar to S. coelicolor putative oxidoreductase SCH35.27 E(): 3.4e-07, 34.8% identity in 282 aa overlap. Contains Pfam match to entry pr00743 FWO-like, Flavin-binding monoxygenase like"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mrrtcvigagpsglaasrvlasrgipedcyeagsgigglwrygn DNGMSGVyasuHaniskesmsfsslpwedsypvphhmyolarlesyaptfglhghig LRTEVTSVRPVEGGGWEVTRRSRGAEAETDRYTEVVVANGHHWDPRLPDPAVPGAGV FEGSAVHAHAYKSSPEPYAGQRVLJVVGMCNSGCELAAEISRSAAKTFLSARAVAHVFPK MLLGRPADHWAVSRAAVLPRFLKDPGMALLLRLARGAPALYGLPEPVRRPLAAHPSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(834. .857)
/gene="SCJ21.02c"
/note="PS00017 ATP/GTP-binding site motif A (P-loop)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="SCJ21.03, probable flavin-containing monooxygenase, len: 458 aa; similar to many eukaryotic monooxygenases, e.g. FMO5_RABIT dimethylaniline monooxygenase [N-oxide forming] (532 aa), fasta scores; opt: 938 z-score: 1016.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(961, .964)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS00017 ATP/GTP-binding site motif A (P-loop) and Pfam match to entry PF00005 ABC_tran, ABC transporter"
                                                                                                                                                                                                             /note="SCJ21.04c, unknown, len: 448 aa; some similarity to M. tuberculosis hypothetical protein TR:P71694 (EMBL:295844) Rv1425 (459 aa), fasta scores; opt: 150 z-score: 166.6 E(): 0.063, 23.9% identity in 464 aa
                                                                                                                                                                                                                                                                                                                                  complement(2660. .4006)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="putative flavin-containing monooxygenase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transporter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="SCJ21.02c"
/note="bf--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=11
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                                                                                                                                                                                          overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                          complement(2660
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAPVSDTV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DELLVQLARGAVTAKPGIRSFGRDSVSFTDGSRETVDAVVYATGYSLSFPFLAPAVFA
APDGRTELYLRTVPPRLPGLFFMGLAQPAGAAFPLLEPQAEWIADLIEGEVLLPTPAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Flavin-binding monooxygenase-like,
7.5e-25"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1194.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RLRDAGRSVLVVSHLAYDIDRLDQLWRLEGGRLHIQERPMEAAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLAFTEYLDQRAGRLSGGSRQKLNLTLALMHDPDVLLLDEPYQGFDWETYLRFWELAT
                                                                                                                           /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                 /gene="SCJ21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTRSTARARERHDKVYAPSYRHGTETDTCAYRRALRRELRAGRRRARRADARRPDAPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="SCJ21.03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="SCJ21.03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   //Octe-"pfam match to entry PF00743 FMO-like, //Octe-"pfam match to entry PF00743 FMO-like, Flavin-binding monooxygenase-like, score 47.90,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="SCJ21.03"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MDVHDVHHSYRQHAVLRGVGLRLKPGTLAGIVGENGAGKTTLLK/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSGELRPDRGTVHHSGRFGYCPQTVVLDDSFTVRQHLDFFRSAFGLTGLERAEEVME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2570
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                                                                                                                                                                                                                                                                                                                                                                                                                              .4006)
                                                               i protein SCJ2.04c"
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E-value 1.9e-40"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E-value
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CDS gene

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Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
22944 GCCGGCTCACAGGCCGACCGCCTGCAGCAGACGGCTCAGGTGGTGGATCTGATCGGCACG 22885
                                                                                                                                                                         23064 ATCACCGCCTCGGACAACACCTGGCTGTACAAGTCGCCGGGCCAGGAACAGCGCGGTCTG 23005
                                                                                                                                                                                                                                                               23124 CCGCCCGCGCCGCGCGCGCACCGCGTGCAGTACGGCACCGCGATCCTTTCGCGCTACCCC 23065
                                                                                                                                                                                                                                                                                                                                                     23184 GCGGAGTTGGCGGAGTTGCTGGGTTACCACGTCGTCTTCGGCGCCCAACATCGACAACAGC 23125
                                                                                        23004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23289 CTGCGGCGTGGCGAACGTCATCCGGAAGAGCGGCGCAGATGTGGTCGGCCTCCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                    33229 GTCGAC-----AAGCACTACTCGGCGCGCGCGAC-----TGGGCGGACCAGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RBS
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                                                                                                                                   531
                                                                                                                                                                                                                                                                                                               495
                                                                                                                                                                                                                                                                                                                                                                                                483
                                                                                                                                                                                                                         512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   447 LeuGluArgSerAlaHisLeuLeuAsnGluThrGlyAlaAspPheIleThrIleLeuGlu 466
                                        550 ---GlyAsnHisGluAspAspLeuAspArgLysLeuGlnAlaIleAlaValSerLysLeu 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               467 SerAspAlaSerLysProTyrMetGlyAsnAsnAspLeuThrMetTrp-----
                                                                                   CTGCATGCCACGCTCGACGTCCACGGCAAGAAGGTGCAGTTCTACAACACGCATCTGGCC
                                                                                                              -----LeuGlyGluLysLeuGlyPheTyrThrAspPheGly------
                                                                                                                                                                                                                  IleValLysSerGluHis---HisLeuLeuProSerProGluGlyGluIleAlaProAla 530
                                                                                                                                                                                                                                                                                                        -----ProSerThrArgTyrHisThrTrpGlyIleMetAlaLeuSerArgTyrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="hypothetical SCJ21.05"
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RTNVEGTRHVLELAAAGREPVRTVGTAFVAGARRRGVAYEDELDDGAGENAYEOS
KYEAELLVHAWSREHGRPALVLRPSILVTDVPSHPELPSHPLQVVERILRDARRATVA
APPTATSSPNGAPDGSSRGAHGLPGPBARRFKVRTVGHPHGRLINLLPVEHAADVMVRLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="SCJ21.05"
4632. .5993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLPVDARRADEEQTWGNRCFALPVDLPVGPAPGRPDGSPDEEAPLRRLDQIMAVTRKL
RGDTWRQAVQDLVRYMPDRPTAWYLRRMLSPRVTNVMATSMPLAEKGSLGETRVTGTA
LLPLLVPGHLCGVGLSFFGDWAEVSFVADRALPLGELLPELWEQAVRELAESVQRG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELPSSHGVDTYHVVHDRDVPVPTVVALLERLVPLSIDLVDAKPEDPSALETMIDFYPG
ITAYLTHRRRFDDTRVRTLLGPAAVCAPVGLDGLWSGLAPRSGALPRPPDSPPAPAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
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141.50
39.13%
24.90%
3.80%
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Matches:
Conservative:
Mismatches:
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Score:

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...mo sapı AL451104 Homo sapi

L4-1104

ALIGNMENTS

RESULT 1 AK025164 PRI 29-SEP-2000 linear 2486 bp AK025164 Homo sapiens cDNA: FLJ21511 fis, clone COL05748. AK025164 LOCUS DEFINITION AK025164
AK025164.1 GI:10437625
oligo capping; fis (full insert sequence).
Homo sapiens colon cDNA to mRNA, clone_lib:COL clone:COL05748.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. ACCESSION VERSION KEYWORDS SOURCE ORGANISM 1 (sites)
Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y.,
Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
NEDO, human,cDNA's equencing project
Unpublished (2000)
2 (bases 1 to 2486)
Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
Direct Submission REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS Direct Submission
Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure Analysis, Human TITLE JOURNAL

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Best Local Similarity
Matches 2100; Conser
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ACTTCACTAAACCCAATCTGGAGTTATCAGATGTCCAACAAAGTGATACTGACATTAAGT
                                   CTCAGAATTTGGGGATTCATTTAGGACAGATTGTTCTTGTTCTACGCATATGGTAT
                                                                                                                                                                                                                                                                                                                                          TCTTCCTCACTGATAGTGCAAGCTGTGACTTGGTGGTCGGGAAGTCATTTGCAAAGGTAC
                                                                                                                                                                                                                                                                                                         CTCTACCATGACCTGGGACCGATGATCTATTACTTTCCTTTGCAAACACTAGAACTCACT
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                                                                                                                                                                                        TGGAAATTGGTTAACAAGAAGTGGATGCTAACCCCTGCTGAGGATAATCACTATTGGCAGC
                                                                                                                                                                                                                                                      GGGCTTGAAGGTTTTAGTATAGCATTTCTTCTCCAATATTCCTAACAATTACTCCTTTC
                                                                                                                                                                                                                                          GGGCTTGAAGGTTTTAGTATAGCATTTCTTTCTCCAATATTCCTAACAATTACTCCTTTC
                                                                                                                                                                                                                                                                                            CTCTACCATGACCTGGGACCGATGATCTATTACTTTCCTTTGCAAACACTAGAACTCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'-& 3'-end one pass sequencing: Departent of Vicology and Human Genome Center, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Tokyo (partly supported by Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEDO human cDNA sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                              692
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mislwrelilesligovswslyhdlgpmiyxfplqileg
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183. .2282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Center: Shirokane-dai, 4-6-i, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
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RYPTYKSEHHLLPSPEGEIAPAITLTVNISGKLVDFVVTHFGNLEDDLDRKLQAIAVS
KLLKSSNQVIFLGYITSAPGSRDYLQLTEHGNVKDIDSTDHDRWCEYIMYRGLIRLG
YARISHAELSDSEIQWAKFRIPDDPTNYRDNQKVVIDHREVSEKIHFNPRFGSYKEGH
YNFNNHWEHNNTDKYNTI"
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/tissue_type="colon"
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/db_xref="taxon:9606"
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                                                         ATGTGGCTAGGGGAAAAGTTGGGTTTCTATACAGACTTTGGTCCAAGCACAAGGTATCAÇ
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                                                                                                                                                                                                                    Direct Submission \mathcal{N} submitted (31-OCT-2001) National Institutes of Health, Mammalian \mathcal{N} submitted (31-OCT-2001) National Institutes of Health, Mammalian \mathcal{N} Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
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BC016523.1 GI:16741399
Web site: http://www.hgsc.bcm.tmc.edu/cdna/Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hul
                                                       Center code: BCM-HGSC
                                                                    DNA Sequencing by: Baylor Sequencing Center
                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert
                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 2412)
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Library Arrayed by: The I.M.A.G.E. Consortiu
Sequencing by: Baylor College of Medicine Hur
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TCTTCCTCACTGATAGTGCAAGCTGTGACTTGGTGGGTCGGGAAGTCATTTGCAAAGGTAC

TCTTCTTCCTTGATAGTGCAAACTGTGACCTGGTGGTCAGGAAGTGGATTGCAAAGGTAC

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GGGCTGGAATTCTTTTGTGTAGCCTTTCTCTCTCCGATACTCTTAACAATTCCCCCACTC GGGCTTGAAGGTTTTAGTATAGCATTTCTTTCTCCCAATATTCCTAACAATTACTCCTTTC

TGGAAATTGGTTAACAAGAAGTGGATGCTAACCCTGCTGAGGATAATCACTATTGGCAGC

TGGAAACTCGTCAATAAGAAGTGGACACTCTCTCTGCTGAGGATCGTCACTGTAGGCAGC

CTCTACCATGACCTGGGACCGATGATCTATTACTTTCCTTTGCAAACACTGAGAACTCACT ATGCCAGGCCTGTGGAGAGCAATTGCCCTGGAGACCTTGCTGGGCTACGTCTCCTGGTCT ATGACCTCGCTGTGGAGAGAAATCCTCTTGGAGTCGCTGCTGGGATGTGTTTCTTGGTCT

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CTCTACCACGGACTGAGCCCCATGATCTATTATTTTCCCCCTGCAAACGCTGGAGCTCACA

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This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                            628
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SLIVQTVTWWSGSGLQRYLKIWGFILGHVLLLVLRIWYTSLNPIWSYQMSNRVLITLS
AVAVLDRIGTDGDYRNPEGKRREVARGRTSLLSWILLPGAARGSLLFLFHWIFGEVSI
VSRWAVSGHHPHGPDRNPFGGAVLLGFSSGLMLSGSSWILDGAGLMWMTGAASAMGLL
VSRWAVSGHHPHGPDRNPFGGAVLLGFSSGLMLSGSSWILDAGLMWMTGAASAMGLL
VLRTWAAAVSGCVLAVFTGSMMPQVLGHLVNSGKNSGEAMATGMILVYLQTFFGAWCT
AFKFYPGGVYARERSDYLLGTIMVIIGLSMLFGPKRNLDFILQTKNSBKTLLRCSEKY
MKLILMLFVGYGLLGLGLRHRTYFEROLGRGAPATVVSAAIWPFRFGYDNEGRWNLERS
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RYPIVRSEHHLLPSPEGEIAPAITMTVNVSNRLVDFVVTHFGNHEDDLDRKLQAIAVS
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model. 10 month old virgin mouse. Taken by biopsy."
/clone_lib="NCI_CGAP_Maml"
/lab_host="DH10B"
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/db_xref="taxon:10090"
/clone="MGC:27925 IMAGE:3584006"
                                                                                                                                                                                                                                  KLLKNCSNQVIFLGYITSEPGSRDYIQLTKHGNVKDIDSSDGDRWCEYIMYRGLIRLG
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/translation="MPGLWRAIALETLLGYVSWSLYHGLSPMIYYFPLQTLELTGLEF
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/protein_id="AAH16523
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4 (bases 1 to 184 Waterston, R.H. Direct Submission Submitted (03-JUL-
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                                                                                                          Swearengen, S. and The sequence of Ho
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tatteno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (07-NOV-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6 On Jul 3, 2001 this sequence version replaced gi:12057004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McPherson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://bacpac.med.buffalo.edu)
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                                                                                                                                                                                                                                                                                                                                           sequence fidelity of RP11-317G22 between bases 17725 to 17956 not be guaranteed due to an unresolved dinucleotide repeat. The uence fidelity of RP11-317G22 between bases 86965 to 87015 can be guaranteed due to an unresolved homopolymeric run.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: sapiens@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ing information for this clone was provided by Dr. John D. erson, Department of Genetics, Washington University, St. For additional information about the map position of this ence, see http://genome.wustl.edu/gsc
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EST AV609860 (NID:g9745530)" (NID:g5853713) wv02e08.x1"

(NID:g3412359) oy39a10.s1"

(NID: 96876448)"

(NID:g1956281)" (NID:g12672693)" (NID:g3802338) gi44g05.x1"

(NID:g2933898) of07d05.s1

(NID:g13544848)" (NID:g12673728)" (NID:g1377608) zd37c01.s1"

(NID:g1956281)"

EST AV609860 (NID: 99745530)"

(NID:g2189572) zx82a02.s1"

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                                               Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                    AL158816 222885 bp DNA
Homo sapiens chromosome 6 clone RP3-405B4,
PROGRESS ***, 33 unordered pieces.
Center:
                                 On Aug 29, 2000 this sequence version replaced gi:9926474
                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 222885)
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Sanger Centre
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                                                                                                                                                    Hominidae;
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*** SEQUENCING IN
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Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; LO8752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality; 204390 bases at least Q40 consensus quality; 211527 bases at least Q30 Consensus quality; 215491 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insert size: 219685; sum-of-contlys Insert size: 126349; 14.0% error; agarose-fp Quality coverage: 3.63x in Q20 bases; sum-of-contlys Quality coverage: 6.72x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: dJ405B4
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runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is
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                                                                       103517 107503
107565 131678; contig of 24114 bp in
107665 131778; contig of 24114 bp in
131779 131878; gap of
100 bp
131779 131878; contig of 3383 bp in
                                     135262 135361: gap of 135362 137913: contig
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103517 107564: contig of 4048
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100202 103416: contig of 3215 bp in
                    137914 138013: gap of
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87340 93671: contig of 6332 bp
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3600 3699: gap of 100 bp
3700 12818: contig of 9119 bp in length
12819 12918: gap of 100 bp
12919 16398: contig of 3480 bp in length
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48536: contig of 14990 bp in length
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31. gap of
18590:
140949: contig
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97550: contig of 3779 bp in
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87239: contig of 4474 bp in
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69090: contig of 3866 bp in
90: gap of 100 bp
73894: contig of 4704 bp in
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55599: contig of 6963 bp in length
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26905: contig of 4433 bp in
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82665: contig of 8671 bp in
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29581: contig of 2576 bp in
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169051 173724: contig of 4674 bp
173725 173824: gap of 100 bp
173825 179991: contig of 6167 bp
173825 179991: contig of 6167 bp
179992 180091: gap of 100 bp
180092 190208: contig of 10117 bp
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27006. .29581
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3700. .12818
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141050. .156466
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138014. .140949
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135362. .137913
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131879. .135261
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Best Local Similarity 89.6%;
Matches 172; Conservative
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                                                                                                                                                                        Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 29, 2000 this sequence version replaced gi:9926474.
Center project name: dJ405B4
------- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; LO8752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
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AL158816.11 GI:9943990
HTG: HTGS_PHASE1; HTGS_CANCELLED
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Homo sapiens chromosome 6 clone RP3-405B4,
PROGRESS ***, 33 unordered pieces.
                                                                                                                                         Center: Sanger Centre
Center code: SC
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                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1. (bases 1 to 222885)
                                                                                                      Contact: humquery@sanger.ac.uk
                                                                                                                      Web site:
                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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164937. .168950
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190309. .193471
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                                                                                                                      http://www.sanger.ac.uk
                                                                                       ···- Project Information
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Pred. No. 1.4e-33;
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Insert size: 219685; sum-of-contigs
Insert size: 126549; 14.0% error; agarose-fp
Quality coverage: 3.63x in Q20 bases; sum-of-contigs Quality
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3699: gap of 100 bp
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190: gap of 100 bp
73894: contig of 4704 bp in length
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7929: gap of 100 bp
222885: contig of 24956 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCCHRIII 316613 bp DNA linear S.cerevisiae chromosome III complete DNA sequence. X59720 S43845 S49180 S58084 S93798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rad,M.R., Lutzenkirchen,K., Xu,G., Kleinhans,U. and Hollenberg,C.P. The complete sequence of a 11,953 bp fragment from C1G on chromosome III encompasses four new open reading frames Yeast 7 (5), 533-538 (1991) 91377317
                                                        Bolle, P.A.,
The complete
                                                                                                                                                               Benit, P., Chanet, R., Fabre, F., Sequence of the sup61-RAD18 rev
                                                                                                                                                                                                                                                                           The complete sequence of a 10.8kb fragment
                                                                                                                                                                                                                                                                                                               Biteau, N., Fremaux, C., Hebrard, S., Menara, A.,
                                                                                                                                                                                                                                                                                                                                                                   of Saccharomyces cerevisiae
Yeast 8 (1), 71-77 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Wilson, C., Bergantino, E., Lanfranchi, G., Valle, G., Carignani, G. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              baker's yeast.
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     Yeast 8 (3),
                                                                                                                              Yeast 8 (2), 147-153 (1992)
                                                                                                                                                Saccharomyces cerevisiae
                                                                                                                                                                                                                                       Yeast 8 (1), 61-70 (1992)
                                                                                                                                                                                                                                                                                                                               (bases 1 to 316613)
                                 le,P.A., Gilliquet,V., Berben,G., Dumont,J. and Hilger,F. complete sequence of K3B, a 7.9 kb fragment between PGK1 and 1 on chromosome III, reveals the presence of seven open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 316613)
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Oliver.S.G., van der Aart.Q.J., Agostoni-Carbone,M.L.,
Alberghina,L., Alexandraki,D., Antoine,G., Anwar,R., Babenit,P. et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            plevani, P. and Lucchini, G.
Nucleotide sequence of 9.2 kb left of CRY1 on yeast chromosome from strain AB972: evidence for a Ty insertion and functional analysis of open reading frame YCR28 Yeast 8 (9), 805-812 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wilson, C., Grisanti, P. and Frontali, L.
The complete sequence of a 6146 bp fragment of Saccharomyces cerevisiae chromosome III contains two new open reading frames yeast 8 (7), 569-575 (1992)
Sequencing project replaced by [13] 17 (bases 1 to 314)
                                                                                                                                                protein Ycr77p
Yeast 11 (6), 581-585 (1995)
95373282
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Sloninski, P.P. and Brouillet, S.
A data-base of chromosome III o
Yeast 9 (9), 941-1029 (1993)
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Nucleotide sequence of D105, a E
chromosome III of Saccharomyces
Yeast 8 (8), 681-687 (1992)
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                                                                         Direct Submission Submitted (16-MAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The complete DNA sequence of yeast chromosome Nature 357 (6373), 38-46 (1992)
                                                          collected by MIPS on
                                                                                                                                                                                                   Rodriguez-Cousino, N., \tilde{L} Lill, R., Neupert, W. and Court, D.A. Identification and initial characterization of the cytos
                                                                                                                                                                                                                                                                                                                                                      93377412
                                                                                                                                                                                                                                                                                                                                                                   Yeast 9 (7), 753-759 (1993)
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Agostoni Carbone, M.L., Panzeri, L., Muzi Falconi, M.,
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                                                          behalf of the European
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, a BamHI fragment
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                                                          Sried, FRG. Data
Yeast Chromosome
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YCL25c-b (C_E13(YCL)27c-a)), PEP Y, new ORF
YCL021w-a (C_C125), PEP Y, new Orf
ALTERED GENETIC ENTITIES:
YCL076w, PEP Y, peptide elongated N-terminally by 51 aa YCL074w,
PEP Y, 3 aa exchanged
YCL075x, PEP Y, 4 aa exchanged
YCL075x, PEP Y, 4 aa exchanged
YCL068c (C_E190->C_E260), PEP Y, peptide elongated N-terminally b
70 aa YCL065w, PEP Y, 1 aa exchanged
YCL061c (C_D853->C_E1096), PEP Y, peptide elongated N-terminally
243 aa YCL051w, PEP Y, 11 aa altered, 6 aa exchanged, 1 aa
additional, 4 aa less at the C-terminus
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Submitted (14-FEB-1995) MIPS, D-8033 Martinsried, FRG. Data
collected by MIPS on behalf of the European Yeast Chromosome
Sequencing project. Update originating from E.J. Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the nt sequence of YCL014w leads elongated polypeptide encoded by Bud3p polypeptide from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences.

on Jul 3, 2001 this sequence version replaced gi:1907116.

on Jul 3, 2001 this sequence version replaced to the file server in The contig sequence which has been released to the file server in 1992 has been subject to a resequencing project, achieved by the joint effort of G. Valles and G. Volckaerts laboratories. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (25-JUN-1993) MIPS, D-8033 Martinsried, FRG. Data collected by MIPS on behalf of the European Yeast Chromosome Sequencing project. Update originating from E.J. Louis revised by [18]
19 (bases 1 to 316613)
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Submitted (28-DEC-1992) MIPS, D-8033 Martinsried, FRG. Data collected by MIPS on behalf of the European Yeast Chromosome III Sequencing project. Update originating from A. Jimenez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            following lines present a summary of the altered entitles. The resequenced chrili contig is 316613 bp with GCG-check: 429 GENETIC ENTITIES valid no longer: YCL012w (YCL014w + YCL012w -> YCL014w / C_B1367 + C_C231->C_A1636).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Resequencing project, achieved by the joint effort of G. Valles and G. Volckaerts laboratories. Munich information center for protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (17-JUN-2001) MIPS Yeast Genome Database, GSF Ingolstaedter Landstrasse 1 D-85764 Neuherberg, Germany,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (29-JAN-1996) R. Gromadka, Protein Biosynthesis Institute of Biochemistry and Biophysics, Pawinskiego 5A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission Submitted (25-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                               single nt exchange resulting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YCR103c (C_F111, former ORF in region corresponding to coord. 307255-307587(C)) is obsolete, open reading frame is destroyed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEP Y, ORF in identical form now C-terminal part of YCR061w. YCR068w-a (YCR068w + YCR068w-a -> YCR068w / C_C429 + C_A145 -> C_A520), PEP Y, ORF in identical form now C-terminal part of YCR068w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YCL006c, PEP Y, ORF obsolete, is not an ORF in current Chromosome III contig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mips-yeast-adm@gsf.de
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21 (bases 1 to 316613)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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20 (bases 1 to 316613)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       replaced by [14]
18 (bases 1 to 316613)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YCR062w (YCR061w + YCR062w -> YCR061w / C_A583 + C_B120 -> C_B631)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL-Entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEP Y, ORF in identical form now C-terminal frame shift in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Poland, Electronic Mail Address: robert@psd.ibb.waw.pl
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                                                                                                                                                                                                                                                                                                                                                                                                                  codon after 45 aa.
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Schizosaccharomyces pombe (strain:PR745) cDNA to mRNA clone_lib:library of H. Nojima clone:SY 0503.
                                                                                           Schizosaccharomyces pombe D89130
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9e-26;
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                                                                            CTCCTGCTATTCATGCAACACTAGATGTCTACGGAGAGCTAATAGATGTTGTGGTTTCTC
                                                                                                                     CACCAGCCATCACATTGACCGTTAACATTTCGGGCCAAGCTGGTGGATTTTGTCGTGACAC
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ACAATGGTCAATATGAAAGTCAGTTGGATCGACGTCTTCAGAGCACTGAGTTGGCTCGAA
                                    ACTTTGGGAACCACGAAGATGACCTCGACAGGAAACTGCAGGCTATTGCTGTTTCAAAAC
                                                                                                                                                           CCAAATTTCCTATTGTCAACTCGACTCACCATTTGTTACCTTCTCCTCAAGGAGAACTTG
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98162722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (15-NOV-1996) Sachiyo Yoshioka, Tsukita Cell Axis ERATO JST, Kyoto Research Park; 17 Chudouji Minamimachi, Shimokyo-ku, Kyoto, Kyoto 600, Japan (E-mail:syoshi@cell.tsukita.jst.go.jp, Tel:+81-75-315-7913, Fax:+81-75-315-6420)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
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/db_xref="GI:1749468"
/db_xref="GI:1749468"
/translation="IYSFASIRISSFYSBAKVWGGAFLVYILYSLAHVWVVAYEFVPG
GPILRERTSYILIFIGWULAALVPAYSGESKEPNKADSSVVDIKQSDSSYRRRSFKKS
LLTGFCLALMALKFAIQNMPPYDYTPYHPNEKLFTAGIWTIHFGLDNFMYASENRIRD
AVRDMELDVFGLLESDTQRLIMGFRDLTQVLAHDLGMYADYGPGPDKHTWGAALLSKF
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MRESPRPLVFLGYVVSNVGQEPQTILTRDTGMLDIEPADYDRWCQYIFYRGVKRIGYA
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/clone="SY 0503"
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/strain="PR745"
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S.pombe
AL355632
                                                                                                                                                                                                              (URL, http://www.sanger.ac.uk/Projects/S_pombe/)
During 1995 to 1996 about 66% of S. pombe chromosome 1 was
sequenced by the Sanger Centre. The sequencing of the S. pombe
genome is now being continued with funding from The European
Commission. Fourteen European sequencing laboratories, including
the Sanger Centre, are participating in the project.
Protein coding regions (CDS) have been predicted with the help of
computer analysis using the Genefinder program in PomBase (an ACEDB
database) with additional predictions for the branch-acceptor sites
supplied by the program Sp3splice. CAUTION: It is possible that for
number of internacional predictions for the branch-acceptor sites
supplied by the program Sp3splice. CAUTION: It is possible that for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (19-APR-2000) European Schizosaccharomyces genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and Katholieke Universiteit Leuven, Laboratory of Gene Technology,
(complementary strand).
The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.
The length in codons is given for each CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL355632.1 GI:7768476 Actin-related protein; cell polarization; coiled-coil; cut9
                                                                                                        number of introns/exons or we may not have chosen splice donor/acceptor sites.

CDS are numbered using the following system eg SPB pombe), B (chromosome 2), c25H2 (cosmid name), .01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Details of yeast sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kardinaal Mercierlaan 92, B-3001 Leuven, Belgium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Robben, J., Volckaert, G., Wood, V.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(1545...1979,2109...2256,2343...2392))
/gene="SPAC688.02c"
complement(join(1545...1979,2109...2256,2343...2392))
/gene="SPAC688.02c"
/note="SPAC688.02c"
/note="SPAC688.02c
                                                                                                                                                                                                                                                                                                                                                                                                                 /note="ttaacatatag, splice branch and acceptor" complement(2103. .2108)
/gene="spac688.02c"
/note="qtgagt, splice donor sequence" complement(2257. .2271)
/gene="spac688.02c"
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                                                                                                                                                                                                                                                                                                       /note="ttaacactttataag,
complement(2337...2342)
/gene="SPAC688.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MSSHGDASYLPKIALESINDYSYYKSYFRQAIQEKLAIHLPEQA
SREAGMGREDQLRIRVKEMLNELIESTFSIIQENVTINGFDANSALQDPKNSDQIEPF
DLALRTRVQQLFNEYEDAHVLVARYRKSYPAQYEKAYYDAMEQQTAFLRNVKDDYVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene-"SPAC688.01"
/note-"SPAC688.01, len:425, SIMILARITY:Saccharomyces
/note-"SPAC688.1, len:425, SIMILARITY:Saccharomyces
cerevisiae, YCQ7_YEAST, hypothetical 107.9 kd protein.,
(953_aa), fasta scores: opt: 1034, E():0, (46.5% identity
                                                                                                              complement(join(2596. .2953,3083. .3297,3381./gene="SPAC688.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="hypothetical protein similar to yeast YCR017C protein involved in sensitivity to certain drugs" /protein_id="CAB90768.1" /db_xref="GI:7788477"
                                                                                                                                                                                         /note="gtgtgt, splice donor sequence"
complement(join(2596. .2953,3083. .32)
/gene="SPAC688.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="SPAC688.02c"
/note="++--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QDKEVENPDEQTSTTVFRKEDIDRYEQTIAKVAYLKKNLPRVVARLEKTP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="hypothetical protein with very low similarity to yeast ypl233w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PESHRYPSLFEGTGVNGHYYDNNLVVHEPWYYD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVSHNGQYESQLDRRLQSTELARIMRESPRPLVFLGYVVSNVGQEPQTILTRDTGMLD
IEPADYDRWCQYIFYRGVKRIGYARLHRSTITDTELQTGKFLVTKDLGRNVRIDKEHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="CAB90769.1"
/db_xref="GI:7768478"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/label=SPAC688.02c
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/label=SPAC688.01
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                                                                          note="SPAC688.03c, len:204, SIMILARITY:Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in 430 aa)"
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/strain="972h-"
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/chromosome="I"
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ammecrl protein., (333 aa), fasta scores: opt:
):3.4e-25, (40.3% identity in 186 aa)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(5637. .6842,6927. .6980))
/gene="SPAC688.06c"
complement(join(5637. .6842,6927. .6980))
/gene="SPAC688.06c"
/note="SPAC688.06c", len:419, predicted to contain coiled-coil region, SIMILARITY:S. cerevisiae, LOW to Actin-related protein, regulator of microtubule stability, YB61_YEAST, (324 aa), fasta scores: opt: 125, E():0.76, (21.3% identity in 300 aa)"
                                                                                                                                                                                                                                                                                                   complement(4164 ...4775)
/gene="SPAC688.04c"
/note="Match to PF00043 GST, Glutathione S-transferases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene-"SPAC688.04c"
/note-"SPAC688.04c, len:242, SIMILARITY:Saccharomyces
cerevisiae, YIVE YEAST, Glutathione transferase GTT1, (234
aa), fasta scores: opt: 274, E():3.5e-11, (27.0% identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="gtatga, splice donor complement(4047. .4775)
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                                                                      PHDYLITSTKTVLEFDDIVTQTHRAISQVVKQAKDNSVWIKILTYSAIÐVEEFQLWLK
RKNLNVSLDLIKSWCDKYGVLMKGSWH"
                                                                                                                                                                                                                                NESDILEPDLNTRVAEDNDVLLSRYSKIKNSASCRNTFEHSAYHSNREËISSSGFYYH
RKPQLFEKSLEKLGNKSIEANRSPLIKELCESANSTENVCFSVSTVDE†QQRHPSAGH
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LSPLGKSPIVDDGVTYIESAAIIEHLVRKYGDSFKPSEEDVAELEKYELMMHFSEAS
LMPFIWASHYLDLSVNMTPIFFRYIVRQFVNGIKSKVLSKETFLULDVIBNHLASNEY
FAGEQFTAADPQMCFPIFAAQRDYLSQKPYKNIKRMMRVVSDRPACRIAAEKVEDNTL
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complement(3298. .3315)
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/gene="SPAC688.03c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(2662. .2953,3083. .3273))
/gene="SPAC688.03c"
                                                                                                                                                     AKSLKEKLENFPVEKLRATAESYGFKSSDSKATLTKTVESCLDATDSR\$QSKKLGKET
                                                                                                                                                                                                 SIDSTCQSNSFLEGDSATHKKKKTDNIKEFTSCEFNDRSRTLLNYAGYMDTNKNADNE
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complement//^^*
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LLECQIDLLYDFEPIDDPLDWEYGIHGVSIKFTANGIRYSSTYLPSVAAEQRWDQEET
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/protein_id="CAB90771.1"
/db_xref="GI:7768480"
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/protein_id="CAB90770.1"
/db_xref="GI:7768479"
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/label=SPAC688.03c
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                                             Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                  Sequence 7987 from Patent WO0194629
AX337478
Young, P.E., Augustus, M., Carter, K.C., Horrigan, S., Soppet, D.R. and Weaver, Z
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                                                                                                                                                                  AX337478
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/note="gtatga, splice donor sequence"
complement(7359..10475)
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complement(6921. .6926)
                                           Metazoa; Chordata; Craniata; Vertebrata;
Butheria; Primates; Catarrhini; Hominidae;
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 /organism="Saccharomyces bayanus"
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                    Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqrefégenoscope.cns.fr) Web: www.genoscope.cns.fr)
This STS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveriny Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S. Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aigle,M. and Durrens,P. Genomic Exploration of the Hemiascomycetous Saccharomyces bayanus var. uvarum FEBS Lett. 487 (1), 37-41 (2000)
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                                                                                                                                                                                                                                                             CCCTACTGACGATGATAGGTGGTGTG-ATATATCTTGTATAAAGATTTGAGAAGACAGGK 989
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                                                                                                                                                                                             990
                                             AC106576
AC106576.1 GI:18139100
                                                                              AC106576 165893 bp DN. Rattus norvegicus clone CH230-198N10, ***, 68 unordered pieces.
                               HTG; HTGS_PHASE1
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1 putative frameshift(s)"
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/variety="uvarum"
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
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                                                                                                                                                                                                                                          Consensus quality: 137306 bases at least Q40 consensus quality: 144043 bases at least Q30 consensus quality: 144604 bases at least Q20 Estimated insert size: 139846; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 2.2x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center clone name: CH230-198N10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
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Barbaria,J.,
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COMMENT

consists of 68 contigs.

The true order of the pieces

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is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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RESULT 13
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Best Local Similarity
Matches 82; Conserv
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                                          CTGCTGTGCTTGGCAAGTGGATTGATGCTTCCATCTTGTTTTGTGGTTTCGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCTGTGGCTGCTTGTTGGTGTGGGATTGTTGGGATTAGGACTACGGCATAAAGCCTATG 1246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAGAAAACTGGGCAAAGTGGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The intronless pseudogene presented below, is missing 317 bases between positions 725 and 726, eliminating the stop codon. The start codon is located at positions 264-266. This gene is flanked by short direct repeats, 'taaattt', suggesting that it is generated by integration of a reverse-transcribed copy of TPI mRNA into germ line DNA via a transposon-like mechanism. A potential poly-A signal is located at positions 1119-1124.
                                                                                                                                                                                                                                                                                                   Xu,J., Skeiky,Y.A., Reed,S.G. and Che Compositions and methods for therapy
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae 1 (bases 1 to 54)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 127 from Patent AX106346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Characterization of the functional gene and several processed pseudogenes in the human triosephosphate isomerase gene family Mol. Cell. Biol. 5 (7), 1694-1706 (1985)
                                                                                                                                                                                                                                                          Patent: WO 0125272-A 127 12-APR-2001; CORIXA CORPORATION (US)
                                                                                                                                                                                                                                                                                                                                                                                                                           AX106346.1
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Brown,J.R., Daar,I.O., Krug,J.R. and Maquat,L.E.
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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upstream of NcoI site.
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/db_xref="taxon:9606"
17 c 9 g
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313 c 304 g
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/db_xref="taxon:9606"
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 54
                                                            Local
AX200497
Sequence 127
AX200497
                                                                                                                                                                                                                            Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W., Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Reed,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., D. Skeiky,Y.A. and Wang,A.
                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 54)
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Sequence 127 from Patent
AX140637
AX140637.1 GI:14280751
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                                                                                                                                                                                                                                                                                                                                              AX200497.1
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1 (bases 1 to 54)
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/db_xref="taxon:9606"
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and Meagher,M.J.
therapy and diagnosis of prostate
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Day,C.H.,
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Search completed: October Job time : 4661 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd

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Scoring table:
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1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
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0. / SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT: *

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4. / SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT: *

5. / SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT: *

6. / SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT: *

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22. / SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT: *

23. / SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT: *

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Listing first 45 summaries
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
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SUMMARIES
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(without alignments)
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	AAK76563	AAK76562	ABL33710	AA160109	AA158323	AAH33952	AAS76980	AAD23551	AAI61370	ABA15594	ABL32150	AAF22291	AAA69168	AAS61363	AAS61226	AAS46468	AAS67909	AAH48024	AAS46427	AAX84253	AAC81736	AAH14130	AAS27442	AAV74374	AAC89559	ABA17139	ABL33218	AAS46417	AAS11614	ABA19235	AAZ80484	ABL33708	AAX13059	AAS72985	ABL24162	AAH02544
			-	Human polynucleoti	Human polynucleoti	Human colon cancer	DNA encoding novel	Human lung tumour-	Soybean 515002 reg	Human nervous syst	Human immune syste	BAC containing rep	Bacteriophage Dp-1	Human gene regulat	Human gene regulat	Tumour suppressor	DNA encoding novel	Internal control B	Tumour suppressor	Human Nck associat	Human secreted pro	Human cDNA sequenc	cDNA encoding nove	Staphylococcus aur	histone dea	nervous sys	Human immune syste	Tumour suppressor	Human genomic DNA	Human nervous syst		Human immune syste	Enterococcus faeca	DNA encoding novel	Drosophila melanog	Prostate tumour an

ALIGNMENTS

RESULT 1 WPI; 2001-639362/73. P-PSDB; ABG02368. 31-MAR-2000; 2000US-0540217. 23-AUG-2000; 2000US-0649167. Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss 13-FEB-2002 AAS66555; Drmanac (HYSE-) HYSEQ INC. 30-MAR-2001; 2001WO-US08631 11-OCT-2001. WO200175067-A2 Homo sapiens DNA encoding novel human diagnostic protein #2359 AAS66555 standard; cDNA; RT, Liu C, (first entry) Tang 635 ВP

Result

NO.

Match

Length DB

IJ

Description

DNA encoding novel

Query

384.8 142.8 Score

2 2 6 B

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AAS66554 AAS66554 AAV61215 AAV6600 AAA06363 AAS63571 AAS10122 AAH93479 AAH84793

DNA encoding novel cDNA sequence of p Prostate tumour sp Human immunogenic

Human prostate tum Human prostate cDN

prostate-spe

New isolated polynucleotide and encoded polypeptides, useful in

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RESULT 2
AAS66554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC for libertifying expressed genes. (I) is useful in gene therapy techniques (C to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC imaging of sites expressing (II). (I) and (II) are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful in treating CC discreters involving aberrant protein expression or biological activity. (C The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed consecution of the coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1693 GTTTCAAAACTACTGAAAAGTAGCTCTAATCAAGTGATATTTCTGGGATATATCACTTCA 1752
               DNA encoding
                                                   13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 635 BP; 255 A; 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention
                                                                                                                        AAS66554 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess bloddversity
                                                                                                                                                                                                                 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                             GCACCTGGCTCCAGAGATTATCTACAGCTCACTGAACATGGCAATGTGAAGGATATCGAC
                                                                                                                                                                                                                   TGAAAACAACCATAATTTTCATATGAATACTCCCCAAATACTTTTTATGAAAC
                                                                                                                                                                                                                                  TGAAAACAACCATCATTTTCATATGAATACT-CCCAAATACTTTTTATGAAAC
                                                                                                                                                                                                                                                                                                      AGTTTCTGAGAAAATTCATTTTAATCCCAGATTTGGATCCTACAAAGAAGAAGACACAATTA
                                                                                                                                                                                                                                                                                                                                                                                                 GATCCCTGATGACCCCACTAATTATAGAGACAACCAGAAAGTGGTCATAGACCACAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                   TATGCAAGAATCT-CCCATGCTGAACTGAGTTCAGAAATTCAGATGGCAAAATTTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCACCTGGCTCCAGAGATTATCTACAGCTCACTGAACATGGCAATGTGAAGGATATCGAC
                                                                                                                                                                                                                                                                                     AGTTTCTGAGAAAATTCATTTTAATCCCAGATTTGGATCCTACAAAGAAGGACCCAATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           {	t AGCACTGATCATGACAGATGGTGTGAATACATTATGTATCGAGGGCTGATCAGGTTGGGT}
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             novel human diagnostic
                                                 (first entry)
                                                                                                                        CDNA; 670
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Pred. No. 1.6
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               protein #2358
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nes 3;
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                                                                                                                                                                                                                                                                                                                                                                           Matches 170; Conserv
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                                            2001
                                                                                                                                      1941
                                                                                                                                                                                                                                    1881
                                                                                                                                                                                                                                                                                                      1821 TCATGACAGATGGTGTGAATACATTATGTATCGAGGGCTGATCAGGTTGGGTTATGCAAG 1880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 670 BP; 181 A; 177 C; 132 G; 180 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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23-AUG-2000;
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                                                                                                                                                                                                           AATCTCCCATGCTGAACTGAGTGAGTTCAGAAATTCAGAATTGCAAAATTTAGGATCCCTGÅ 1940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-639362/73
DB; ABG02367.
                      GAAAATTCATTTTAATCC
                                                                                        TGACCCCACTAATTATAGAGACAACCAGAAAGTGGTCATAGACCACAGAGAAGTTTCTGA 2000
                                                                                                                                                                                                                                                                                TCAGGTTATTACCTGTCTTTTAAATACGCTTCGGATAGTTACAAGGTTGGGTTATGCAAG 408
                                                                                                                                                                                     AATCTCCCATGCTGAACTGAGTGATTCAGAAATTCAGATGGCAAAATTTAGGATCCCTGA
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2000US-0649167.
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                                         2018
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Pred. No. 2e
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RESULT 4
AAV58600/c
ID AAV58600;
XX
AC AAV58600;
XX
DT 08-DEC-1998 (first
XX
DE Prostate tumour spec
XX
DE Prostate tumour spec
XX
DE Homo sapiens.
XX
PN WO9837418-A2.
XX
PD 27-AUG-1998.
XX
PF 25-FEB-1998; 98WO
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AAV61215/c
ID AAV612
XX AAV612
XX AV612
XX O6-JAN
DT O6-JAN
DE CDNA S
XX Prosta
XX Prosta
XX Homo s
XX Homo s
XX PN WO9837
XX
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25-FEB-1997;
01-AUG-1997;
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                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptides comprising immunogenic portions of prostate proteins used in a vaccine for the treatment of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA sequence of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV61215 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP
                                                                                                Prostate tumour specific gene; human; prostate
                                                                                                                                                                                                                                                                                                                                             tissue
                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                   present sequence is a new DNA which encodes an immunogenic portion a prostate tumour protein. The encoded immunogen, or the DNA itself, be used as a vaccine for the treatment of prostate cancer. The DNA identified by analysis of a subtracted cDNA library obtained by tracting a prostate tumour cDNA expression library with a normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1998-609886/51
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                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer;
                                                                                                                                                                                                                                                                                                                                           a prostate
library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xu J;
                                                                                                                                                                                                                                                                             2.6%;
llarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                       BP; 23 A;
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97US-0806099.
97US-0904804.
     98WO-US03690.
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                                                                                                                     specific
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Pred. No.
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                                                                                                                                                                                                                                                                                       DB 19; ; 3.1e-06;
                                                                                                                                                                                                                                                                                                                       other;
                                                                                                                                                                                                                                                                               0;
                                                                                                cancer; detection;
                                                                                                                                                                                                                                                                                                 Length 54;
                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                         777
                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                             Gaps
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RESULT 5
AAA06363/c
ID AAA06363 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-FEB-1998;
25-FEB-1997;
01-AUG-1997;
                                                                                14-JUL-1998;
14-JUL-1998;
23-SEP-1998;
23-SEP-1998;
23-SEP-1999;
15-JAN-1999;
15-JAN-1999;
09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents a human prostate tumour specific gene, and can be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as encoded by this sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dillon
                                                                                                                                                                                                                                                                                  Human immunogenic prostate tumour protein cDNA sequence
                                                                                                                                                                                                                                                                                                                             AAA06363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-480805/41.
                   WPI; 2000-171268/15.
                                                                                                                                                                   14-JUL-1999;
                                                                                                                                                                                        27-JAN-2000
                                                                                                                                                                                                             WO200004149-A2
                                                                                                                                                                                                                                                                Human;
                                                                                                                                                                                                                                                                                                        13-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human prostate specific tumour protein for detecting and treating prostate cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP
                                                            (CORI-)
                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                     Human; prostate cancer;
immunogenic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                 724 CTGCTGTGCTTTGGCAAGTGGATTGATGCTTCCATCTTGTTTTGTGGTTTTCGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                      54
                                                                                                                                                                                                                                                                                                                                                                                                      CTGCTGTGCTTGGCAAGTGGATTGATGCTTCCATCTTGTTGTTGTTGTTGTGGT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
54; Conserv
                                       Š,
                                                            CORIXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 95; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ×
                                       Harlocker
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0904809.
97US-0806596.
97US-0904809.
                                                                                                             98US-0115453.
98US-0116134.
98US-0159812.
98US-0159822.
                                                             CORP
                                                                                99US-
                                                                                                      99US:
                                                                                                                                                                   99WO-US15838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 A; 17 C; 9 G; 5 T; 0 other;
                                                                                                                                                                                                                                                               cancer; diagnosis; tumour;
                                                                                5-0232149.
5-0232880.
5-0288946.
                                                                                                                                                                                                                                                                                                                                                  cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.6%;
                                       SL,
                                                                                                                                                                                                                                                       vaccine;
                                                                                                                                                                                                                                                                                                                                                  54
                                      Yuqiu
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 54; DB; Pred. No. 3.1
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                  ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 19;
3.1e-06;
                                       ŗ
                                                                                                                                                                                                                                                               gene
                                        Mitcham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and
                                                                                                                                                                                                                                                                therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 54,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                        JL
                                                                                                                                                                                                                                                                                    SEQ
                                                                                                                                                                                                                                                                 detection;
                                                                                                                                                                                                                                                                                                                                                                                                                           777
                                                                                                                                                                                                                                                                                    ID NO:127.
                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prostate
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New polypeptide useful for treating and

diagnosing prostate cancer

comprises an immunogenic portion of

prostate tumor protein

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X A
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AAS63571/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the polypeptides, antibodies against the polypeptides and vaccines comprising them can be used for inhibiting the development of prostate cancer in a patient. The polypeptides can be used to generate antibodies or anti-idiotypic antibodies for passive immuno therapy. A portion of the polypucleotides encoding the polypeptides can be used as a probe or to, modulate the expression of the polypeptides can be used as a probe or the polypeptides can be used as a probe or to, modulate the expression of the polypeptides. AAA06241 to AAA06591 and AAV82000 to AAV82020 represent sequences used in the exemplification of the present invention.
                                                                                                         Fanger GR,
Li SX, Wan
                                                                                                                                                                                                                                                                09 MAY - 2000;
12 MAY - 2000;
13 JUN - 2000;
27 JUN - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes isolated polypeptides, comprising an immunogenic portion of a prostate tumour protein (PTP). The polypeptides and polynucleotides encoding them have cytostatic activity and can be used in vaccines and in gene therapy. The polypeptides and
          Claim 1;
                                                                                                                                                                                                                                                                                                                      27-MAR-2000;
                                       the
                                                   New
                                                                                                                                                                                                                                                                                                                                                                               04-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                           WO200173032-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human prostate cDNA sequence #123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JAN-2002
                                                                                                                                                                                              10-OCT-2000;
                                                                                                                                                                                                                                       10-AUG-2000;
29-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                   27-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS63571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS63571 standard; cDNA; 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
                                                                                                                                                                 (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 724 CTGCTGTGCTTGGCAAGTGGATTGATGCTTCCATCTTGTTGTGGTTTCCTGGT 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54; CT6CT6T6CTT6GCAA6T6GATT6AT6CTTCCATCTT6TTTGT6GTTTC6T6GT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                       SEP-2000;
                                                                                                                                                                                                                                     AUG-2000;
                                    human prostate-specific polypeptides and polynucleotides useful diagnosis and treatment of cancer, especially prostate cancer -
                                                                                2001-639232/73.
                                                                                                       Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 BP; 23 A; 17 C; 9 G; 5 T; 0 other;
           Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 143;
                                                                                                                                                                                           2000US-0568100
2000US-0570737
2000US-0593793
2000US-0605783
2000US-0636215
2000US-0657279
2000US-0657279
2000US-0659426
2000US-0685166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                   2001WO-US09919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                         2000US-0536857
          274; 579pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 21;
. 3:1e-06;
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                                                                                                                        Carter
                                                                                                                                   Kalos
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                                                                                                                      r MD;
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                                                   for
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δÃ

Matches Query Match

Local

Similarity

100.0%;

2.68;

Score 54; pred. No.

DB 22; I

Length

54

Conservative

0;

Mismatches

0;

Indels

0

Gaps

0

777

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AAS10122/c
ID AAS10122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific polynucleotide of the invention.
 Sequence
                          The sequence is a human prostate tumour cDNA which encodes a partial tumour protein. The DNA is useful for inhibiting the development of prostate cancer or for treating prostate cancer in a patient.
                                                                                       Example 2;
                                                                                                                   Novel polynucleotide encoding polypeptide comprising a portion of prostate tumour protein useful for inhibiting development of prostate cancer or for treating prostate cancer in a patient -
                                                                                                                                                                                                                                                                                      25-FEB-1997;
01-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                           US6262245-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human prostate tumour cDNA #13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS10122;
                                                                                                                                                                               WPI; 2001-440862/47.
                                                                                                                                                                                                             Хu J,
                                                                                                                                                                                                                                                                        09-FEB-1998;
                                                                                                                                                                                                                                                                                                                                 25-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated prostate-specific
                                                                                                                                                                                                                                          (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                             17-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                724 CTGCTGTGCTTGGCAAGTGGATTGATGCTTCCATCTTGTTGTTGTGGTTTCGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                             Dillon
 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 BP; 23 A; 17 C; 9 G; 5 T; 0 other;
                                                                                          Column 137;
 BP; 23 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                     97US-0806099.
97US-0904804.
98US-0020956.
                                                                                                                                                                                                                                                                                                                                   98US-0030607
                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumour protein; prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA;
17 C; 9 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.6%;
                                                                                       105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; 1
3.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0:
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RESULT 8
AAH93479/c
ID AAH93479 standard; cDNA; 5/
XX
AC AAH93479;
XX
DT 04-OCT-2001 (first entry)
XX
DE Human prostate-specific cD)
XX
KW Human; prostate cancer; processor concerned by the con
RESULT 9
AAH84793/c
ID AAH847
XX
AC AAH847
XX
AC AAH847
XX
25-SEP
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                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) can be used for monitoring the progression of cancer in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotide encoding a prostate-specific protein, diagnosing, monitoring and treating prostate cancer in a for use in vaccines -
    25-SEP-2001
                                        AAH84793;
                                                                             AAH84793 standard;
                                                                                                                                                                                                                                                                                                                                         Sequence 54
                                                                                                                                                                                                                                                                                                                                                                              exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                 (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93944 and AAM01115 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 272; 543pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-425873/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kalos MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JAN-2000; 2000US-0483672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-JAN-2001; 2001WO-US01574.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200151633-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human prostate-specific cDNA sequence P126
                                                                                                                                                                                                                                                                                                                                                                                                   AAM01318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORI-) CORIXA CORP
                                                                                                                                                                                                  724 CTGCTGTGCTTGGCAAGTGGATTGATGCTTCCATCTTGTTTTGTGGTTTTCGTGGT
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4
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                                                                                                                                                                            CTGCTGTGCTTGGCAAGTGGATTGATGCTTCCATCTTGTTTTGTGGTTTCGTGGT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGCTGTGCCTTGGCAAGTGGATTGATGCTTCCATCTTGTTTTGTGGTTTCGTGGT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dillon DC, Mitcham JL, MD, Fanger GR, Day CH,
                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                            represent polynucleotide and amino acid sequences used in the ication of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Meagher MJ;
                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                         BP; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer; prostate-specific;
e therapy; metastasis; ss.
                                                                               CDNA;
                                                                                                                                                                                                                                                                                                                                       A; 17 C; 9 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                2.6%;
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                                                                               54
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                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                              Score 54;
Pred. No.
                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                            DB 22;
3.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis; vaccine;
                                                                                                                                                                                                                                                                                              Length 54;
                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    patient and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for
                                                                                                                                                                                                                  777
                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                              AAH02544/c
ID AAH025
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-308785/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kalos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-NOV-1999;
18-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200134802-A2
  12-APR-2001
                                        WO200125272-A2
                                                                                                                                                                                                                  14-JUN-2001
                                                                                                                                                                                                                                                       AAH02544;
                                                                                                                                                                                                                                                                                                AAH02544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                             Homo
                                                                                                                                                                                                                                                                                                                                                                                                54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dillon DC, Mitcham JL, HMD, Retter MW, Stolk JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 BP; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   325pp; English.
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09-NOV-2000; 2000WO-US30904
                                                                                                                                                                                                                                                                           prostate specific antigen; PSA; ss.
                                                                                                                                                                                                                                                                                             Human; prostate cancer; therapy; diagr chromosome 22q11.2; prostate-specific
                                                                                                                                                                                                                                                                                                                                                    Human prostate-specific cDNA sequence P126
                                                                          99US-0439313
99US-0443686
                                                                                                                                                                                                                                                                                                              diagnosis;
                                                                                                                                                                                                                                                                                             protein;
                                                                                                                                                                                                                                                                                                              cat
 Jiang Y,
                                                                                                                                                                                                                                                                                              chromosome 1;
Reed SG;
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Isolated polypeptide comprising at least prostate-specific protein, useful in the Harlocker SL, Jiang Y ,, Day CH, Skeiky YAW, an immunogenic diagnosis and t c portion therapy o Wang A;

The present invention describes an isolated polypeptide (P1) comprising at least an immunogenic portion of a prostate-specific protein, or its variant. Also described are polypuroleotides (N1) encoding (P1). (P1) and (N1) have cytostatic activity and can be used in vaccine production. The polypeptides, nucleic acids and antibodies from the present invention are useful in the diagnosis and therapy of prostate cancer. Prostate specific genes P704p, P712p, P774p, P775p and B305D are located in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome region. Prostate specific antigen (PSA) P501S was located on thromosome 1, AAH84571 to AAH85143 and AAG9900 to AAG9907 represent polynucleotide and polypeptide sequences used in the exemplification of the present invention. the present invention.

A; 17 C; 9 G; 5 T; 0 other;

Conservative 2.6%; 5cc. 100.0%; Pr Score 54; DB; Pred. No. 3.1 DB 22; .1e-06; Length 54; Indels 0 Gaps 0;

724 CTGCTGTGCTTGGCAAGTGGATTGATGCTTCCATCTTGTTTTGTGGTTTTCGTGGT 777

Human; prostate tumour antigen; prostate tumour; therapy; diagnosis; prostate cancer; immunogenic; cytostatic; vaccine; ss. Prostate tumour antigen determined cDNA sequence for P126 (first entry) cDNA; 54 ВP

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RESULT 11
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    at least an immunogenic portion of a prostate tumour antigen protein its variant. (I) have cytostatic activity and can be used in vaccine production. (I), prostate tumour antigen polynucleotides, an antigen presenting cell (APC e.g. a dendritic cell) that expresses (I), and a pharmaceutical composition containing (I) are useful for inhibiting the development of cancer in a patient. Antibodies specific for prostate specific proteins and ollogonucleotides that hybridise to a polynucleotide that encodes a prostate specific protein are useful for detecting the presence or absence of a cancer or monitoring the progression of a cancer, especially prostate cancer. AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes an isolated polypeptide (I) comprising
 New isolated nucleic acid genes from Drosophila and
                                             WPI; 2001-656860/75
                                                                                                                             23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                      23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                       Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                  Drosophila; developmental
                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster genomic polynucleotide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                             ABL24162 standard; DNA; 7850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prostate specific protein and its encoding polynucleotide, useful the treatment and diagnosis of prostate cancer - \,
                                                                                                                                                                                                   27-SEP-2001
                                                                                                                                                                                                                             WO200171042-A2
                                                                                                                                                                                                                                                                                    pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                         26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                724 CTGCTGTGCTTGGCAAGTGGATTGATGCTTCCATCTTGTTTTGTGGGTTTCGTGGT 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 CTGCTGTGCTTGGCAAGTGGATTGATGCTTCCATCTTGTTTTGTGGTTTCGTGGT 1
                                                                                                 ) PE
                                                                       JC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 BP;
                                                                                                   CORP
                                                                    Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                             2000US-191637P
2000US-0614150
                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                   NY.
                                                                                                                                                                                                                                                                                   gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; 17 C; 9 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reed SG,
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                                                                       PWD,
detection reagent for detecting for elucidating cell signalling
                                                                                                                                                                                                                                                                                                biology;
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Pred. No.
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                                                                     Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                  cell signalling;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22;
. 3.1e-06;
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                                                                                                                                                                                                                                                                                                  insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling a cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA seguences (ABLIG175) and the encoded proteins
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                     31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                 30-MAR-2001;
                                                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic,
food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS72985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                              p-PSDB;
                                                                                                                                                                                                                                                11-OCT-2001
                                                                                                                                                                                                                                                                            WO200175067-A2
                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding novel human diagnostic protein #8789
                                                                                                                                                                                                                                                                                                                                                                                                                 13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS72985 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1250 GAAAACTGGGCA 1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1070 TGTTAATTATCGGGCTGAATATGCTATTTGGTCCTAAGAAAAACCTTGACTTGCTTCTTC 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7850 BP; 1994 A; 1770 C; 1831 G;
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                                                                                                                                       (HYSE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 1.8%;
Local Similarity 50.0%;
                                                             2001-639362/73
DB; ABG08798.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAATGTGTTCA 6005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGTAGATGGTAGCACTTCTTTGAGTATTAAGTAATGGCTTTGTTCATCTATAGACTGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTTCCAAATCAGATAAGCGGAGGTTTGAAGTAAATGTGCATAATCCTTGCAAATTAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAACAAAAAACAGTTCTAAAGTGCTTTTCAGAAAGAGTGAAAAATACATGAAAACTTTTTTC 1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTGGCTGCTTGTTGGTGTGGGATTGTTGGGATTAGGACTACGGCATAAAGCCTATGAGA
                                                                                                                                       HYSEQ
                                                                                                          RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 23959; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                     2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                         Liu C,
                                                                                                                                                                                                                  2001WO-US08631
                                                                                                                                       INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA;
                                                                                                         Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2523
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                      forensic;
                  mutations
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biodiversity

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RESULT 13
AAX13059/C
ID AAX130
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AC AAX130
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DT 19-MAR
DT 19-MAR
CONTROL Entero
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PD 12-NOV
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PR 16-MAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC for identifying expressed genes. (I) is useful in gene therapy techniques (CI). (II) is useful for generating antibodies against it, detecting or cyantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical considers involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess blodiversity amino acid sequences. AAS64197-AAS94564 represent novel human considers in the sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO careful activity and in the printed considers of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
   14-NOV-1997;
06-MAY-1997;
16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy technique.
                                                                                                                                                                  Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated polynucleotide (I) and
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                                                                   04-MAY-1998;
                                                                                                    12-NOV-1998
                                                                                                                                     WO9850555-A2
                                                                                                                                                                                                    vaccine;
                                                                                                                                                                                                                                                     Enterococcus
                                                                                                                                                                                                                                                                                      19-MAR-1999
                                                                                                                                                                                                                                                                                                                       AAX13059
                                                                                                                                                                                                                                                                                                                                                      AAX13059 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                    Enterococcus faecalis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGGGCCAGCATCTGCAGAAACGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAGAAGTCTCTCTTGTTTCCAGATGGGCAGTGAGTGGGCATCCACATCCAGGGCCAGAT 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGCTGGTGTCCTTGCTGGTGGTGGCATGTGCTTGCCATGCCATGCCAGCAGATCTGGG
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                                                                                                                                                                                                   attenuation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2523 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ID No
                                                                                                                                                                    faecalis
                                                                                                                                                                                                                                                 faecalis genome contig SEQ
   97US-0066009.
97US-0044031.
97US-0046655.
                                                                   98WO-US08985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      526 A; 803 C; 669 G;
                                                                                                                                                                                                                                                                                                                                                      DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8789; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.8%;
                                                                                                                                                                                                   ; contig;
computer
                                                                                                                                                                                                                                                                                                                                                      9813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                       ВP
                                                                                                                                                                                                                  detection;
                                                                                                                                                                                                    readable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        525 T; 0 other;
                                                                                                                                                                                                      medium;
                                                                                                                                                                                                                                                     ID NO:122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 23;
                                                                                                                                                                                                                    Enterococcal infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        819
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ID ABL337
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                                                                                                                                                                                                                                                                                                      RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. AAX12938 to AAX13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1166
                                                                                                                                                                                                                                                                                                                                                 2567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2747
                                               antiinflammatory; cancer; eye disease; arter acute myeloid leukaemia; Alzheiner's disease neurofibromatosis; rheumatoid arthriticagene. Ac
                                                                                                                                                                                                                                                                                                                                                                                                                                               1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barash SC,
                                                                                                     neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                 Human; immune system disease; cytosine methylation; antiasthmatic;
antiarteriosclerotic; antianaemic; cytostatic; nootropic;
                                                                                                                                                                               Human
                                                                                                                                                                                                                                                                        ABL33708 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                            gene;
                                                                                                                                                                                                              26-MAR-2002
                                                                                                                                                                                                                                          ABL33708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAAAAACCTTGACTTGCTTCAAACAAAAAAACAGTTCTAAAGTGCTTTTCAGAAAGA 1165
                                                                                                                                                                                                                                                                                                                                                    AGGGTAATACTTGCACTCGGTGGTGT
                                                                                                                                                                                                                                                                                                                                                                               CTGCTGCCATCTGGCCTTTCAGGTTT 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAATAAAGGAGAAAAACTTTCGTTTTTCTCCTTAGTTTTCTTTGCATTTTTTGTTTTTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGAAAAATACATGAAAACTTTTTCTGTGGCTGCTTGTTGGTGTGGGATTGTTGGGATTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGACCATGACAACCACTCGGCGATAAATATTGACTAATAAGAATAAACCAATAAAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101;
                                                                                                                                                                               immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                               system
                                                                                                                                                                                                              (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       734-739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3233 A;
                                                                                                                                                                                                                                                                          DNA;
                                                                                                                                                                               associated gene SEQ ID
                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38; Pred. No.
                                                                                                                                                                                                                                                                          ВP
                                                         eimer's disease; AIDS;
arthritis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2161
                                                                                        arteriosclerosis; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G; 2719 T; 2 other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                          disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
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                                                                                                                                                                                                                                                                                                                                                                                                                 2568
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RESULT 15
AAZ80484
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                    6044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1970
                                                                                                Human; gene expression product; diagnosis; tumour; colon cancer; colorectal adenocarcinoma; cell line SW480; cell proliferation; cytostatic; sarcoma; breast cancer; neoplasia; dysplasia;
                                                                                                                                                                                                                                                                                                                                                   2090
                                                                                                                                                                                                                                                                                                                                                                               6104
                                                                                                                                                                                                                                                                                                                                                                                                          2030
                                                                                                                                                                                                                                                                                                                                                                                                                                       6164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6533 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         macular degeneration, arteriosclerosis, anaemia, cancer, acute mye leukaemia, Alzhelmer's disease, AIDS, epilepsy, neurofibromatosis, rhemmatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 1681; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-130909/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-2000;
01-SEP-2000;
16-DEC-1999
                            WO9964576-A2
                                                       Homo sapiens
                                                                                    hyperplasia;
                                                                                                                                                            Human colon cancer
                                                                                                                                                                                         07-APR-2000
                                                                                                                                                                                                                                               AAZ80484 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6224 AAACTACAATAAAAAATCATACTATCACCAAACAACACGCACATTATTTTTTAACCGAAA 6165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-Jul-2001; 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200200928-A2
                                                                                                                                                                                                                                                                                                                      AATTTATTTAATA
                                                                                                                                                                                                                                                                                                                                                   ACTTTTTATGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAATTCAGATGGCAAAATTTAGGATCCCTGATGACCCCACTAATTATAGAGACAACCAGA 1969
                                                                                                                                                                                                                                                                                                                                                                               CCAACAAAAAATAACAAATAATAAAAAAACCAAAATTTCTTAAAAACACGCACTTAA
                                                                                                                                                                                                                                                                                                                                                                                                         CCTACAAAGAAGGACAATTATGAAAACAACCATCATTTTCATATGAATACTCCCAAAT 2089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGTGGTCATAGACCACAGAGAAGTTTCTGAGAAAATTCATTTTAATCCCAGATTTGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                     ds.
                                                                                                                                                                                      (first entry)
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2000DE-1043826
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                                                                                                                                                                                                                                                                                                                      6032
                                                                                                                                                                                                                                                                                                                                                   2102
                                                                                                                                                         cell line SW480 cDNA clone SEQ ID NO:568
                                                                                                                                                                                                                                               cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.8%;
                                                                                                                                                                                                                                                 616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37.8;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 6533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene, useful
abnormal
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                                                                                                                                                                                                                                                                                                                                                                              6045
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Search completed: October 21, Job time : 400 secs

2002, 19:03:07

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Best Local Similarity
Matches 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Endege WO,
Carroll E,
Schlegel R;
                                                                                                                                                                                                                          AAZ79917 to AAZ80766 represent double stranded cDNA clones isolated from the human colorectal adenocarcinoma (colon cancer) cell line SW480. The cDNA clones can be used to generate antisense oligonucleotides which can be used for antisense therapy. Methods and products from the present invention can be used for identifying and/or classifying cancerous cells present in a human tumour, particularly in solid tumours, e.g. carcinomas and sarcomas, e.g. breast or colon cancers. The cDNA clones can be used for developing agents for the diagnosis and treatment of disorders involving unwanted cell proliferation, such as neoplasia,
                              1166
                                                                                          1106
                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acids, used to develop products i treatment of disorders involving unwanted cell particularly cancers, especially colon cancer
                                                                                                                                                                                   Sequence 616 BP;
                                                                                                                                                                                                                  dysplasia or hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                   Claim 15; Page 356; 469pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-087220/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (FARB ) BAYER
350
                                                            290
                 GTGAAAAATACATGAAACTTTTTCTGTGGCTGCTTGTTGTTGTGGGAT 1213
GTCATTAACACTAAAATTCTTTTCTTNNGAAGTTTCTTCTTTTCCGAT 397
                                                            AGACAGATCTGGTTTACCATCTTTTAACAAAAGGCAAATGTCTTCTTCTTCTTCAGAAAGA 349
                                                                                         AGAAAAACCTTGACTTGCTTCTTCAAACAAAAAAACAGTTCTAAAGTGCTTTTCAGAAAGA 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Steinmann KE, Astle JH, Catino TJ, Derti A, For
                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0088801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-IB01062
                                                                                                                                                                                  145 A; 142 C; 163 G;
                                                                                                                                    1.8%;
                                                                                                                       0
                                                                                                                                    Score 37.2;
Pred. No. 1.
                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JH, Burgess CC, Bus
Ford DM, Lewis ME,
                                                                                                                                                                                   144 T;
                                                                                                                                                     DB
                                                                                                                       45;
                                                                                                                                                    21;
                                                                                                                                                                                   22 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                             for
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                                                                                                                                                    Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosis
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                                                                                                                                                     616;
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Result
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       irched:
   on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
   seq length:
seq length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/FB_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    383533 seqs, 122816752 residues
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2103
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US-08-232-463-7
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US-08-942-562-7
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US-08-441-104A-8
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US-09-362-473-3
US-09-116-194-1
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	/ Match Local Simi nes 54;	NUMBER OF SEQUENCES: 178 CORRESPONDENCE ADDRESS: ADDRESSE: SEED and BERRY LLP STREET: 6300 COLUMBIA Center, 7(CITY: Seattle STATE: WA COUNTRY: USA ZIP: 98104 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/020,99 FILING DATE: 09-FEB-1998 CLASSIFICATION: APPLICATION UNMBER: 31,392 REGISTRATION UNMBER: UNMBER: 31,392 REGISTRATION:)-956-12 e 127, NO. 626 AL INFOR ICANT: ICANT:	31.8831.8831.8831.8831.8831.8831.8831.8
CTGCTGTGCTTGGCAAGTGGATTGATGCTTCCATCTTGTTGTGGTGTTTCGTGGTTTCGTGGTTTCGTGGTTTCGTGGTTTCTTGTTG	ilarity Conser	MEQUINCEMEQUIN	7/c Applica 1562 MATION: Xu, Jil Xu, Jil	
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICAT: DILLON, COMPOUN
TITLE OF INVENTION: COMPOUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (206) 682-60 INFORMATION FOR SEQ ID NO:
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
                                                                             APPLICANT:
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REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
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UNREAT APPLICATION DATA:
PROFITS APPLICATION DATA:
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM:
                                                                                                                                                                                                                        INFORMATION:
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o. 6329505
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Fanger, Gary
Retter, Mark
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                                                                                                                         Reed, Steven G.
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CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: Fast-SEQ for Windows Version 3.0
SEQ ID NO 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
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NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMPLECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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ADDRESSEE: Foley & Lardner
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CLASSIFICATION: 435
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SYSTEM: PC-DOS/MS-DOS
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                                                                                      ; NAME/KEY: misc_feature; LCATION: (1)...(616)
; OTHER INFORMATION: n = A,T,C or US-09-328-111-568
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                                                                                                                                                                                          SOFTWARE: FastSEQ for
SEQ ID NO 568
LENGTH: 616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                              Matches
                                                          Query Match
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EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
                                                                                                                                                                                                                                                                                                             APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/328,111
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                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
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                                                                                                                                                  FEATURE:
                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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                                              Similarity
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Catino, Theodore J
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Pred. No. 0.18;
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APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                            NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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1100
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NAME: BENT, Stephen A
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TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
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CLASSIFICATION: 435
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Best Local Similarity
Matches 60; Conserv
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APPLICATION NUMBER: 08/10/94
FILING DATE: 08/10/94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/
FILING DATE: 03/18/94
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APPLICANT:
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OPERATING SYSTEM: PC-D
SOFTWARE: WinPatin (Ge
CURRENT APPLICATION DATA:
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                                                                    1215 AAAGGGCTCCTTGAGGAAGTGGCCATTGATGGTCTGGTTGGCTGTGCCCAGTGGGTTTTT 1156
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CORRESPONDENCE ADDRESS:
640 GGAGAAGTCTCTTGTTTCCAGATGGGCAGTGAGTGGGCAT 681
                                                                                                                580 AACTGGCTGCTGGCAGGGGCTGCTTTTGGTAGCCTTGTGTTCCTCACCCACTGGGTTTTT 639
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                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: Nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Torchia, PhD., Timothy E. REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0873P2
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Urfer, Roman
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                                                                                                                                                                                                          1.7%;
ilarity 58.8%;
Conservative
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                                                                                                                                                                                                          Score 34.8; DE Pred. No. 1.7; 0; Mismatches
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US-08-457-880A-7/c
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Best Local Similarity 58.88;
Conservative
                                                                                                                                                            Sequence 7, Application US/08457880A Patent No. 5910574
                                                                                                                                           GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
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APPLICANT:
                                 TITLE OF INVENTION: HUMAN trk | TITLE OF INVENTION: INHIBITORS NUMBER OF SEQUENCES: 41
                                                                                   APPLICANT: Leonard G. I
APPLICANT: David L. She
APPLICANT: Roman Urfer
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NAME: Torchia, PhD., Timo
REGISTRATION NUMBER: 36,7
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                           640 GGAGAAGTCTCTCTTGTTTCCAGATGGGCAGTGAGTGGGCAT
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ADDRESSEE:
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T: 460 Point San Bruno Blvd
South San Francisco
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David L. Shelton
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Genentech,
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Pred. No. 1.7;
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COMPUTER READABLE FORM:

COUNTRY:

USA

South San Francisco California

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Best Local Similarity
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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                                 SOFTWARE: WinPatin (Ge
CURRENT APPLICATION DATA:
                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: US/0:
FILING DATE: 19-May-1995
APPLICATION NUMBER: 08/2:
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NAME: TOICHLA, PID., TINOTHY E.
REGISTRATION UNMBER: 36,700
REFERENCE/DOCKET NUMBER: P0873P
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APPLICATION NUMBER: US/08/444,622A FILING DATE: 19-May-1995
                                                                                                                                                         COUNTRY:
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David L. Shelton
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Pred. No. 1.
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Best Local Similarity
Matches 60; Conserv
                                                                                                                                                                              APPLICATION NUMBER: US/08/942,56
FILING DATE: 01-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/444,597
FILING DATE: 19-May-1995
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
                                                      TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
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                                       SEQUENCE CHARACTERISTICS:
                                                                                                           TELEPHONE: 415/225-8674
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                                                                                                                                         NAME: Torchia, PhD., Timothy E. REGISTRATION NUMBER: 36,700 REFERENCE/DOCKET NUMBER: P0873P
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STRANDEDNESS: Single
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                  LENGTH:
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Urfer, Roman
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Pred. No. 1
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US-09-156-923-7/c
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Patent No. 6153189
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                                                               Matches
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                                                                                                                                                                                                      TELEFAX: 949/760-9502
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1155
1215. AAAGGGCTCCTTGAGGAAGTGGCCATTGATGGTCTGGCTTGGCCTGTGCCCCAGTGGGTTTTT 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: WinPatin (Ge
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: GE TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                 FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                               580 AACTGGCTGGCAGGGGCTGCTTTTGGTAGCCTTGTGTTCCTCACCCACTGGGTTTTT 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1
CLASSIFICATION:
                                                                                                                                                                        TYPE: Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 10-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/3 FILING DATE: 20-DEC-1994
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                                                              Local Similarity 58.8 es 60; Conservative
                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                      TELEPHONE:
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                                                                                                                                             POPOLOGY:
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                                                              Score 34.8; DE Pred. No. 1.7; 0; Mismatches
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Pred. No. 1.7;
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US-08-286-846A-5/c
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                                                  RESULT 14
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Sequence 5, Apprix
No. 5844092
Sequence 5, Application US/08286846A Patent No. 5877016
                                                                                                                                                                                                                                                     Query Match
Best Local :
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INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: 0
FILING DATE: 03/18/94
                                                                                                                                                                   1215 AAAGGGCTCCTTGAGGAAGTGGCCCATTGATGGTCTGGTTGGCTTGCCCCAGTGGGTTTTT 1156
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: 0
FILING DATE: 08/10/94
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                  640 GGAGAAGTCTCTTGTTTCCAGATGGGCAGTGAGTGGGCAT 681
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                                                                                                                                                                                                  580 AACTGGCTGCTGGCAGGGGCTGCTTTTGGTAGCCTTGTTTCCTCACCCACTGGGTTTTT 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Torchia, PhD., Time REGISTRATION NUMBER: 36 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/01
FILING DATE: 20-Dec-1994
                                                                                                                                                                                                                                     Local Similarity 58.8%; nes 60; Conservative
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Shelton, David L.
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                                                                                                                                                                                                                                    Score 34.8; DB 2;
Pred. No. 2.1;
0; Mismatches 42
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GENERAL INFORMATION:
APPLICANT: Presta,
APPLICANT: Sheltor

Presta, Leonard G. Shelton, David L.

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: TITLE OF INVENTION:

41

Roman

Human trk Receptors and Neurotrophic Factor Inhibitors

ADDRESSEE:

E: Genentech, Inc. 460 Point San Bruno Blvd

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Best Local Similarity
Matches 60; Conserv
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                                                                                                                                                                                                                                                                                                                                                        tent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 2715 base pair
            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb i
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5 inch, 1.44 mb f
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TOPOLOGY: Li
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CLASSIFICATION: 435
                                                                                                                                                   CITY: South San Francisco
STATE: California
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TELEFAX: 415/952-9881
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o. 5910574
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DEDNESS: Single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: U
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ALIGNMENTS

REFERENCE AUTHORS TITLE BASE COUNT ORIGIN VERSION KEYWORDS RESULT 1 BG696417 LOCUS FEATURES COMMENT SOURCE ACCESSION DEFINITION ORGANISM source cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) [Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: mRNA sequence. BG696417 BG696417 1010 bp mRNA linear EST 07-MAY-2001 602659516F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4802907 5', Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 1010) Homo sapiens BG696417.1 High quality sequence stop: 803. Contact: Robert Strausberg, Ph.D. Unpublished (1999) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian http://image.llnl.gov Plate: LLAM10697 row: o column: 318 Ċ) /Clone="InAGE: 4802907"
/Clone=lib="NCI_CGAP_Skn3"
/lab_host="DH10B (Tl phage resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
/note="SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 208 c 230 g 254 t /organism="Homo sapiens" /db_xref="taxon:9606" GI:13961539 .1010 Craniata; Vertebrata; Catarrhini; Hominidae. 04 M.D. Gene Hominidae; Collection (MGC) Euteleostomi; (LLNL) DNA ьe

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                    TTGGAGAGTGATGCTTCTAAGCCCTATATGGGGAACAATGACTTAACCATGTGGCTAGGG
                                                                                                    TCTAGTCTAGAAAGATCAGCTCACCTGCTCAATGAAACAGGTGCAGATTTCATAACAATT 1392
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Plate: LLAM10334 row: j column: 02
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Tissue Procurement: Gilbert Smith,
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
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National Institutes of Health,
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Site_2: Not1; Cloned unidirectionally. Primer: Oligo
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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/strain="FVB/N"
/db_xref="taxon:10090"
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/dev_stage="10 months, virgin"
/lab_host="DH10B"
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National Institutes of Health, M
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Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies,
CDNA Library Arrayed by: The I.M.A.G.E. Conso
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                                                                                /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Saite_2: NotI; Cloned unidirectionally. Primer: Oligo of Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"

247 c 247 g 235 t
                                                                                                                                                                           /organism="Mus musculus"
/strain="FYB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5355137"
/clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/dev_stage="5 months"
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CTGGGTTAGCCTGGTGGGTTCCCGGGCCACTTTCGGGCCGGGGTTCCCCT
                    CTGGTTTGATCTGGTGGGTTACAGGAACAGCTTCAGCTGCGGGGCTCCT
                                                               GTACTGCTGCTTGGCAAGTGGATTGATGCTTCC--ATCTTGTTGTGGTTTCGTGGTA
                                                                                    GCTTTTGGTAGCCTTGTGTTCCTCACCCACTGGGTTTTTTGGAGAAGTCTCTCTTGTTTCC
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                                          GCTCTACTGGGCTTCTCAAGTGGACTTGTGCCAACGGGGTTCACCATGGGTTCCTGGATG
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 4 BI854920 LOCUS REFERENCE DEFINITION BI854920 7 603381910F1 NCI_CGAP_Mam6 mRNA sequence. BI854920 BI854920.1 house mouse

GI:15995667 748 . Mus bp mRN. Craniata; Ver Sciurognathi; CDNA Vertebrata; thi; Muridae; linear EST 10-OCT-2001 Clone IMAGE:5397050 5', Euteleostomi; ; Murinae; Mus

mRNA

Mus musculus Eukaryota; Metazoa; Chordata; Craniata; V Eukaryota; Metazoa; Chordata; Sciurognath Mammalia; Eutheria; Rodentia; Sciurognath 1 (bases 1 to 748) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)

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             ATATTTCTGGGATATATCACTTCAGCACCTGGCTCCAGAGA-TTATCTACAGCTCACTGA 1787
                                                                        GACAGGAAGCTACAGGCTATTGCAGTTTCAAAACTGCTGAAAAATTGTTCAAAATCAAGTG
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Tissue Procurement: Jeffrey Green M.D.
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Contact: Robert St
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Site_2: NotI; Cloned unidIrectionally. Primer: Oligo of
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
162 c 207 g 181 t
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/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
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/db_xref="taxon:10090"
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Pred. No. 6.5e-127;
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                                     GAACAGCTTCAGCTGCGGGGCTCCTTTACCTGCACACATGGGCAGCTGCTGTGTCTGGCT 862
GAGCAGCTTCGGCCATGGGTCTCCTCTACCTGCGCACATGGGCAGCTGCTGTTTCTGGAT
                                                                      GACTGATGCTATCGGGTTCATCATGGCTTCATGATGCTGGGTTAGCCTGGTGGATGACAG 121
                                                                                                                                                    CCCCACCCAGGCCCGATCCTAATCCTTTTGGAGGTGCGGTTCTACTGGGCTTCTCAAGTG 61
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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http://image.llnl.gov
plate: LLAMI1104 row: p column:
plate: ''.'. sequence stop: 739.
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Tissue Procurement: Gilbert Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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602892888F1 NCI_CGAP_Lu29 Mus
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Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                       providing
a 165 c
                                                                                                                                                                                                                                                                                                                       /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

165 c 205 g 209 t
                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic Stem cell origin."
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="CZECH II (feral)"
/db_xref="taxon:10090"
/clone="MAGE:5037956"
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81.1%;
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Pred. No. 2.3
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FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 116 row: N column:
                                                                                                         Contact: Smith TPL
USDA, ARS, US Meat Animal
PO Box 166, Clay Center, N
Tel: 402 762 4366
Fax: 402 762 4390
                                                               Single pass sequencing. Bases (v0.980904.e. Vector identified
                                                                                                                                                                                                                    and
                                                                                                                                                                                                                                                                                                                            EST.
                                       PCR PRimers
                                                                                           Email: smith@email.marc.usda.gov
                                                                                                                                                                           Unpublished (2000)
                                                                                                                                                                                     Design and use of two EST discovery in swine
                                                                                                                                                                                                                              Fahrenkrug, S.C., Freking, B.A., Stone, R.T., Heaton, M.P., Gross
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Fahrenkrug, S.C., Fr
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
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                                                                                    mRNA sequence.
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B1651562.1 GI
         Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 678)
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http://mgc.nci.nih.gov/.
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Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
a 132 c 124 g 144 t
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/db_xref="taxon:9823"
/clone_lib="MARC 2PIG"
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                                                                                                                                                        TCTGGCTGTGTCTTCGCCATCTTTACTGCATCCATGTGGCCCCAAACACTTGGACACCTT 915
                    GAAATATTTTTCTGCCCTGGTGCACAGCTTTTAAGTTTGTCCCAGGAGGTGTCTACGCT
                                                                              ATTAACTCAGGGACAAACCCTGGGAAAACCATGACCATTGCCATGATATTTTATCTTCTA 975
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                                                                                                                                    TCTGGATGTGTCCTGGCAGTCTTTACGGGGTCTATGTGGCCTCAAGTACTTGGCCATCTT
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 676. Location/Qualifiers
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/clone="IMAGE:5338688"
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/db_xref="taxon:10090"
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/lab_host="DH10B"
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Pred. No. 6.3e-116;
0; Mismatches 133;
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                                                ACAGGAAACTGCAGGCTATTGCTGTTTCAAAACTAC-TGAAAAGTAGCTCTAATCAAGTG 1728
                                                                                     TTTCCAACAGACTGGTGGACTTTGTCGTGACCCATTTTGGGAATGACGAAGATGACCTCG
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372176 MA
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Fax: 402 762 4390
Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Single pass sequencing. Bases ov v0.980904.e. Vector identified
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Stone, R.T., Heat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Design and use of two pooled tissue normalized cDNA libraries for
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Library made from pooled tissue from testis,
endometrium, hypothalamus, pituitary, and pli
134 c 126 g 145 t 1 others
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/tissue_type="pooled"
/lab_host="DH10B"
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/db_xref="taxon:9823"
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Eutheria; Cetartiodactyla; Suina; Suidae;
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Pred. No. 1.2e-113;
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                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM10334 row: j column: 03
High quality sequence stop: 653.
Location/Qualifiers
1 066
                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 966)
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                                        254
                                                                                                   /organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="thAGE:4488290"
/clone_lib="NCI_CGAP_Maml"
/clone_lib=""tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
                                    /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sa
Site_2: Not1; Cloned unidirectionally. Primer: Oligo:
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
204 c 262 g 245 t 1 others
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vt53b05.rl Barstead
clone IMAGE:1166769
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AA710301
                                                                                                       Mammalia;
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CCAAAGAGGTCTCTGCCTGCCATCTGGCCTTTCAGGTTTTGGATATGACAATGAAGGGTGGT 1333
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B. Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Rodentia; Sciurognathi; Muridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                       597 bp mRNA linear EST 24-DEC-1997 use irradiated colon MPLRB7 Mus musculus cDNA similar to TR:P78781 P78781 FISSION YEAST;,
                                                                                                                                                                                                                         Muridae;
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                                                                                               ATGCTGAACTGAGTGATTCAGAAATTCAGATGGCAAAATTTAGGATCCCTGATGACCCCA 1948
                                                                                                                                                                                      GATGGTGTGAATACATTATGTATCGAGGGCTGATCAGGTTGGGTTATGCAAGAATCTCCC 1888
   CCAATTACAGAGACAACCAGAAAGTCGTCATAGACCACCGAGGAGTTCCCCAAGAACATTC
                                                                         ATGCAGAACTGAGTGACTCTGAGATTCAGATGGCCAAATTCAGGATCCCGGATGATCCCCG
                                                                                                                                                 GATGGTGTGAGTACATCATGTACCGGGGTCTGATCAGGTTGGGCTATGCAAGAATCTCTC
                                                                                                                                                                                                                             ATTACATACAACTCACAAAACATGGCAACGTGAAGGATATTGACAGCTCAGATGGAGACA
                                                                                                                                                                                                                                                              ATTATCTACAGCTCACTGAACATGGCAATGTGAAGGATATCGACAGCACTGATCATGACA 1828
                                                                                                                                                                                                                                                                                                                           AAAGTAGCTCTAATCAAGTGATATTTCTGGGATATATCACTTCAGCACCTGGCTCCAGAG
                                                                                                                                                                                                                                                                                                                                                                               GGAATCATGAAGATGACCTTGACAGGAAGCTACAGGCTATTGCAGTTTCAAAACTGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                     GGAACCACGAAGATGACCTCGACAGGAAACTGCAGGCTATTGCTGTTTCAAAACTACTGA 1708
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCATAACCATGACAGTTAACGTCCCAACAGAÇTGGTGGATTTTGTGGTGACACACATTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCATCACATTGACCGTTAACATTTCGGGCAAGCTGGTGGATTTTGTCGTGACACACTTTG
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Washin-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Feax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
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141 c 144 g 138 t
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/dev_stage="8 weeks"
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                     CATGGCAATGTGAAGGATATCGACAGCACTGATCATGACAGATGGTGTGAATACATTATG 1848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tissue Procurement: Christopher Moskaluk, M.D., Emmert-Buck, M.D., Ph.D.
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Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                             /note-"Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco;RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 132376-132391, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo.
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/clone_lib="NCI_CGAP_Kidl1"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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1 (bases 1 to 528)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtm12.p1?t1=&t2=PM3-HT0627-270
300-001-e03&t3=2000-03-27&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence tags
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          /note-"Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0627"
/dev_stage="Adult"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence
BI853011
                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu
cDNA Library Preparation: Life Technologies, Inc
cDNA Library Arrayed by: The I.M.A.G.E. Consortion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            603379834F1 NIH_CGAP_Mam3 Mus musculus
                                                                                                                                                                                         DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                              High quality sequence stop:
Location/Qualifiers
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Plate: LLAM11993 row
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/organism="Mus musculus"
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/clone="IMAGE:5389784"
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/lab_host="DH10B"
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                                                                                                                 617 bp mRNA linear EST 20-AUG NCI_CGAP_Utl Homo sapiens cDNA clone IMAGE:2508415 TR:978781 P78781 FISSION YEAST ;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
Contact: Robert Strausberg, Ph.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Primates; Catarrhini; Hon
1 (bases 1 to 617)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 407.
Location/Qualifiers
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Seq primer: -40UP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
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              656 bp mRNA linear EST RIKEN full-length enriched, adult male urinary cDNA clone 9530064017 5', mRNA sequence.
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Site_2: NotI; Cloned unidirectionally. Primer: Oilgo dT.
Average insert size 1.75 kb. Life Technologies catalog #:
11538-014"
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/Clone_lib="NCI_CGAP_Utl"
/tissue_type="well-differentiated
adenocarcinoma, 7 pooled tumors"
/lab_host="DH10B"
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EST.
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
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The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K., Arakawa,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara v. and Hamphirat V.
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
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,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sa
,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.
,Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Project of Genome Exploration Research Group in Riken
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/dev_stage="adult"
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subsequently enriched for full-length by went through one round of normalization subtraction to Rot • 370.0. Second
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                                                 ACTTCACTAAACCCAATCTGGAGTTATCAGATGTCCAACAAAGTGATACTGACATTAAGT
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                                 ACATCATTAAACCCAATTTGGAGCTATCAGATGTCCAACAGAGTAATTCTGACATTGAGT
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Pred. No. 3.9e-88;
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Search completed: October Job time: 2493 secs 21, 2002, B ρy B δÃ Ъ δÃ 밁 Qγ 망 Qy

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RESULT 1

بالأمل والأماء الأربال أما وحال بالأخليج فكالووو والأخيار والمجاهد وها المؤسل المعاملة وماله فيجه يوياسي المعارض

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Q9H720
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                                           PRT:
                     PRELIMINARY;
      Q9H720
ID
      O9H720;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
O1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CDNA: FLJ21511 fis, clone COL05748.
HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Hominidae; Homo.
McMmmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606:
AC
os
OC
OC
       NCBI_TaxID=9606;
οх
 RN
       SEQUENCE FROM N.A.
      TISSUE-COLON;
Kawabata AA, Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AK025164; BAB15080.1;
SEQUENCE 699 AA; 78565 MW; 2F839563189A0523 CRC64;
 RC
 RA
 RA
 DR
   Query Match 99.8%; Score 3713; DB 4; Length 699; Best Local Similarity 99.9%; Pred. No. 3.6e-263; Matches 698; Conservative 1; Mismatches 0; Indels
                                                                                     Gaps
          .1 MTSLWREILLESLLGCVSWSLYHDLGPMIYYFPLQTLELTGLEGFSIAFLSPIFLTITPF 60
         .1 MISLWREIDLESLIGCVSWSLYHDLGPMIYYFPLQTLELTGLEGFSIAFLSPIFLTITFF 60
'1 MTSLWREILLESLLGCVSWSLYHDLGPMIYYFPLQTLELTGLEGFSIAFLSPIFLTITPF 60
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         121 LRIWGFILGQIVLVVLRIWYTSLNPIWSYOMSNKVILTLSAIATLDRIGTDGDCSKPEEK 180
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               KVAPTKEVSAAIWPFRFGYDNEGWSSLERSAHLLNETGADFITILESDASKPYMGNNDLT 480
   Oγ
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                LVDFVVTHFGNHEDDLDRKLQAIAVSKLLKSSSNQVIFLGYITSAPGSRDYLQLTEHGNV 600
    Qу
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    Db
                 DHREVSEKIHFNPRFGSYKEGHNYENNHHFHMNTPKYFL 699
            Qy
     Db
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

October 21, 2002, 21:56:53 ; Search time 63 Seconds (without alignments) 1919.420 Million cell updates/sec Run on:

US-09-809-638-2 3720 1 MTSLWREILLESLLGCVSWS.........EGHNYENNHHFHMNTPKXFL 699 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

562222 seqs, 172994929 residues Searched:

562222 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

C.processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_19:* Database :

sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:* sp_human:* sp_invertebrate:* sp_mammal:* sp_mhc:* sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:* sp_archea:*
sp_bacteria:*
sp_fungi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			3 ID Description	1 Q9H720 Q9h720 homo sapien		3 Q9P6M4 schizosacch		9 Q9HDZ2 schizosacch	Q9s1z5	Q950t2	P95556	079569	11 Q91VY8 mus musculu		5 Q9GJX7 sus scrofa	17 Q9UYP5 pyrococcus	3 Q36149 Q36149 trachemys s	3 Q9B6Y4 casuarius b	
			h DB	9	9	5 3	1 3	8	9 2	3 8	6 2	8	6	9 9	3 6	9	1 8	5 8	7
			Lengt	69	69	42	40	99	27	28	39	9	269	63	64	16	59	9	4.2
	æ	Query	Match Length DB	99.8	84.0	17.2	16.8	6.9	3.8	3.5	3.5	3.3	3.3	3.3			3.3	3.3	۲
			Score	3713	3125	639	625.5	256	141.5	132	128.5	124	123.5	122	122	122	121.5	121	119
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18		3.2	449	7	Q9RL05	
19		3.2	605	æ	095720	
20	•	3.2	613	œ	Q94SY9	Q94sy9 crenimugil
21	118.5	3.2	694	7	Q9L179	
22	117.5	3.5	583	ນ	017069	•
23	117	3.1	604	æ	Q9B6Z4	
24	116.5	3.1	570	œ	Q9B510	
25	116.5	3.1	613	œ	Q94SZ9	-
26	116	3.1	605	æ	Q9B6W0	
27	116	3.1	605	œ	Q9B6U8	dromaius
28	116	3.1	605	ω	Q958A0	Q958a0 dromaius no
29	115.5	3.1	290	17	096xc0	
30	115	3.1	317	16	Q97K74	
31	115	3.1	603	œ	Q9MR50	Q9mr50 ciconia cic
32	115	3.1	603	œ	Q958D4	Q958d4 tinamus maj
33	114.5	3.1	603	ω	Q9GA20	₽
34	114.5	3.1	829	10	Q9LMJ1	Q91mj1 arabidopsis
35	114	3:1	395	7	Q9Z404	Q9z404 pseudomonas
36	114	3.1	909	ω	Q9TA19	Q9tal9 loxodonta a
37	114	3.1	1201	16	Ф9ни70	Q9hu70 pseudomonas
38	113.5	3.1	276	~	O9ZBN3	
39	113.5	3,1.	605	œ	0957x8	
40	113	3:0	604	œ	Q9B6X2	
41	113	3.0	689	13	Q9W701 .	Q9w701 xenopus lae
42	112	3.0	438	10	Q92U86	Q9zu86 arabidopsis
43	111.5	3.0	295	16	Q92T98	
44	111	3.0	4	17	Q9HQN5	വ
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RESULT 1 09H720	Q9H720 PRELIMINARY; PRT; 699 AA	01-MAR-2001 01-MAR-2001	01-MAR-2001 (TrEMBLrel, 16, Last	CDNA: FLUZISII FIS, CLONE COLUS/48. Homo sapiens (Human).		<pre>Mammalia; Eutheria; Primates; NCBI TaxID=9606;</pre>		SEQUENCE FROM N.A.		Okitani R., Ota T.,			Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.			Query Match 99.8%; Score 3713; DB 4; Length 699; Best Local Similarity 99.9%; Pred. No. 2.7e-266;	vative 1; Mismatches 0; Indels 0;	1 MTSLWREILLESLLGCVSWSLYHDLGPMIYYFPLQTLELTGLEGFSIAFLSPIFLTITPF	1 MISLWREILLESLLGCVSWSLYHDLGPMIYYFPLQTLELTGLEGFSIAFLSPIFLTITPF	61 WKLVNKKWMLTLLRIITIGSIASFQAPNAKLRLMVLALGVSSSLIVQAVTWWSGSHLQRY	61 WKLVNKKWMLTLLKIITIGSIASFQAPNAKLRLMVLALGVSSSLIVQAVTWWSGSHLQRY	121 LRIWGFILGQIVLVVLRIWYTSLNPIWSYQMSNKVILTLSAIATLDRIGTDGDCSKPEEK	121 LRINGFILGQIVLVVLRIWYTSLNPIWSYQMSNKVILTLSAIATLDRIGTDGDCSKPEEK
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                                              VÉLCLASGLMLPSCLWFRGTGLIWWVTGTASAAGLLYLHTWAAAVSGCVFAIFTASMWPQ
                                                                         TLGHLINSGINPGKTMTIAMIFYLLEIFFCAWCTAFKFVPGGVYARERSDVLLGTMMLII
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         GLNMLFGPKKNLDLLLQTKNSSKVLFRKSEKYMKLFLWLLVGVGLLGLGLRHKAYERKLG
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Kyaptkevsaaiwpfregydnegwsslersahllnetgadfitilesdaskpymgnndlt
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
KTGEVATGMASRPNWLLAGAAFGSLVFLTHWVFGEVSLVSRWAVSGHPHPGPDPNPFGGA
                                                                                                                                                             WWLGEKLGFYTDFGPSTRYHTWGIMALSRYPIVKSEHHLLPSPEGEIAPAITLTVNISGK
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
IMILAR TO HYPOTHETICAL PROTEIN FLJ21511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84.0%; Score 3125; DB 11;
82.8%; Pred. No. 8.5e-223;
tive 41; Mismatches 79;
                                                                                                                                                                                                                                                                                                       DHREVSEKIHFNPRFGSYKEGHNYENNHHFHMNTPKYFL 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
SEOUENCE 699 AA; 78179 MW; 4F41975D6570D5F8
                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Strausberg R.;
Submitted (OCT-2001) to the
EMBL; BC016523; AAH16523.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 82.8
Matches 579; Conservative
                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                us musculus (Mouse)
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                     KTGEVATGMASRPNWLLAGAAFGSLVFLTHWVFGEVSLVSRWAVSGHPHPGPDPNPFGGA
                                                                                                                                                               301 TLGHLINSGTNPGKTMTIAMIFYLLEIFFCAWCTAFKFVPGGVYARERSDVLLGTMMLII
                                                                                                                                                                                  GLIMLFGPKKNLDLLLQTKNSSKVLFRKSEKYMKLFLWLLVGVGLLGLGLRHKAYERĶLG
                                                                                                                                                                                                                                                                                                                                                                                                                  MWLGEKLGFYTDFGPSTRYHTWGIMALSRYPIVKSEHHLLPSPEGEIAPAITLTVNISGK
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Aert R., Robben J., Volckaert G., Wood V., Rajandream M.A.,
Barrell B.G.;
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EMBL; AL355632; CAB90768.1; -.
Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL 48.6 KDA PROTEIN (FRAGMENT).
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; Pred. No. 3.6e-39;
70; Mismatches 178
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34.2%;
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nes 152; Conservative
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P78781;
01-MAY-1997
01-JAN-1998
                                                                                                                                                                                                                                                                                                                    EMBL; DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1997 (TrEMBLrel. 03, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN PROTEIN (FRAGMENT).
Schizosaccharomyces pombe (Fission yeast).
Schizosaccharomycetales; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                              DNA Res.
                                                                                                                                                                                                                                                                                                                                                            CDNAS
                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98162722;
Yoshioka S., Kato
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces.
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             532
                                                                                                                     416
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TLTVNISGKLYDFYVTHFGNHEDDLDRKLQAIAVSKLLKSSSNQVIFLGYITSAPGSRDY | ::: | :: | | : : | | | | |
                                                                                                                                                                                                                     INSGTNPGKTMTIAMIFYLLEIFFCAWCTAFKFVPGGVYARERSDVLLGTMMLIIGLNML 365
                                      LIMGFRDLTQVLAHDLGMYADYGPGPDKHTWGAALLSKFPIVNSTHHLLPSPQGELAPAI
                                                    PYMGNNDLTMWLGEKLGFYTDFGPSTRYHTWGIMALSRYPIVKSEHHLLPSPEGEIAPAI
                                                                                                                                            ALVPAYSGESKEPNKADSSVVDIKQSDSSYRRRSFKKS-----LLTGFCLALMALKFAIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FYRGVKRIGYARLHRSTITDTELQTGKFLVTKDL-----GRNVRIDKEHVPESHRYPSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYRGLIRLGYARISHAELSDSEIQMAKFRIPDDPTNYRDNQKVVIDHREVSEKIHFNPRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LDRKLQAIAVSKLLKSSSNQVIFLGYITSAPGSRDYLQLTEHGNVKDIDSTDHDRWCEYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRYHTWGIMALSRYPIVKSEHHLLPSPEGEIAPAITLTVNISGKLVDFVVTHFGNHEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HFGLDNFMYASENRIRDAVRDMELDVFGLLESDTQRLIMGFRDLTQVLAHDLGMYADYGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RFGYDNEGWSSLERSAHLLNETGADFITILESDASKPYMGNNDLTMWLGEKLGFYTDFGP
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                                                                                        {\tt NMPPYDYTPYHPNEKLETAGIWTIHFGLDNFMYASENRIRDAVRDMELDVFGLLESDTQR
                                                                                                                                                                                              ISSFYSPAKVWGGAFLVYILYSLAHVWVVAYEFVPGGPILRERTSYIL----IFIGWNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGTGVNGHYYDNNLVVH--EPWYY
                                                                                                                ERKLGKVAP----TKEVSAAIWPFRFGYDNEGWSSLERSAHLLNETGADFITILESDASK
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                                                                                                                                                                                                                                                                                                                               D89130;
                                                                                                                                                                                                                                                                Similarity
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19130; BAA13792.1;
                                                                                                                                                                                                                                                                                                        401 AA;
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                                                                                                                                                                     -GPKKNLDLLLQTKNSSKVLFRKSEKYMKLFLWLLVGVGLLGLGLRHKAY
                                                                                                                                                                                                                                                                                                                                                                      PubMed=9501991;
K., Nakai K., Okayama
f open reading frames :
                                                                                                                                                                                                                                                                                                        45758 MW;
                                                                                                                                                                                                                                                  16.8%; Score 625.5; DB 3; 35.5%; Pred. No. 3.3e-38; tive 63; Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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RESULT
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Best Local
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Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence
Q1-MAR-2001 (TrEMBLrel. 16, Last annotati.
HYPOTHETICAL 77.5 KDA PROTEIN (FRAGMENT).
SPAC589.12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wood V., Rajandream M.A., Barrell B.G., Aert | Weltjens I., Grymonprez B., Volckaert G.; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9HDZ2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein NON_TER 688 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Weltjens I., Grymonprez B., Submitted (JAN-2001) to the EMBL; AL512496; CAC19769.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales; Schiz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schizosaccharomyces pombe (Fission yeast). Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4896;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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675
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                                                                                                                                                                                                                                                                                                                                                                         EVYLSFVFWSVLTSLGLLVWYFPLWHMGISGYEACILFELSPFLLGIPLLRKFASKVPVI
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                       VGVGLLGLGLR
                                                                            VLLGTMMLIIGLNMLF-----
                                                                                                                                                                        FGGAVLLCLASGLMLPSCLWFRGTGLIWWVTGTASAAGLLYL-HTWAAAVSGCVFAIFT-
                                                                                                                                                                                                            VEHFKLRKITA----
                                                                                                                                                                                                                                                                                                                    FL--FLNVIGIAAYKLEDPVHRLFVTAF----SVCCECLAWTSLFSNISPENLAIERKIS
                                                                                                                                                                                                                                                                                                                                               TLLRITTIGSIASFQAPNAKLRLMVLALGVSSSLIVQAVTWW-----SGSHLQRYLRIW 124
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TGFCLALMALK
                                                  YIL----IFIGWNLAALVPAYSGESKEPNKADSSVVDIKQSDSSYRRRSFKKS----
                                                                                                     IYSFASI-----RISSFYSPAKVWGGAFLVYILYSLAHVWVVAYEFVPGGPILRERTS
                                                                                                                                                          HGAVSIVVSICAVLVAPYLYQSGAFMLIGFVLACFGSYFMYINHGWCSYLGGLIFTSYVL
                                                                                                                                                                                                                                      PEEKKTGEVATGMASRPNWLLAGAAFGSLVFLTHWVFGEVSLVSRWAVSGHPHPGPDPNP
                                                                                                                                                                                                                                                                 TFLFGLLASSIAKYSFFSNNPIWPILNETNGGKQIPALIVGIIACLIFAIFHVQQTTANA
                                                                                                                              ---ASMWPQTLGHLINSGTNPGKTMTIAMIFYLLEIFFCAWCTAFKFVPGGVYARERSD
                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
97; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                688 AA;
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685
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77474 MW;
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Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 256; DB 3;
Pred. No. 1.5e-10;
                                                                           -GPKKNLDLLLQTKNSSKVLFRKSEKYMKLFLWLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3985EAC23CDA34FF CRC64;
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Q950T2
ID Q950T2
AC Q950T7
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DT 01
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OS H
OC EN
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Best Local S
Matches 63
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Q9S1Z5;
                                                                01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                               Q95OT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-A3(2);
Seeger K.J., Harris
Submitted (AUG-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
PUTATIVE SECRETED PROTEIN.
          Eukaryota;
                      Mitochondrion.
                                 Hyaloraphidium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97000351; PubMed-8843436; Redenbach M., Kieser H.M., Denapa Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parkhill J., Barrell
Submitted (AUG-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-A3(2);
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NCBI_TaxID=82268;
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                                                                                        -DEC-2001
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et of ordered cosmids and a detailed genetic a
a Mb Streptomyces coelicolor A3(2) chromosome.
Microbiol. 21:77-96(1996)
Microbiol. 21:77-96(1996)
Microbiol. 21:77-96(1996)
Microbiol. 21:77-96(1996)
                                                       DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                      ---PSTRYHTWGIMALSRYPIVKSEH-HLLPSPEGEIAPAITLTVNISGKLVDEVVTHF-
                                                                                                                                                                                                                                                                                                                                                                             LERSAHLLNETGADFITILESDASKPYMGNNDLTMW-----LGEKLGFYTDFG-----
                                                                                                                                                                                                                                                                                                          PPAPGGHRVQYGTAILSRYPITASDNTWLYKSPGQEQRGLLHATLDVHGKKVEFYNTHLA
                                                                                                                                                                                                                                                                                                                                                      LRRVANVIRKSGADVVGLQEVD--KHYSARSD---WADQPAELAELLGYHVVFGANIDNS
                                                                                                                                                                                             KVVIDHREVSEKI
                                                                                                                                                                                                                                         DRWCEYIMYRG-----

    AASDHRPLLGKV

                                                                                                                                                                                                                   DAWAKSLHARGDGATYPAQSPTERIDLIYAT - - - RRVTPLVAQVLK - - - - DDP - - - - -
                                                                                                                                                                                                                                                                AGSQADRLQQTAQVVDLIGTRKPG----ILVGDFNALPAAPE----
                                                                                                                                                                                                                                                                                  -GNHEDDLDRKLQAIAVSKLLKSSSNQVIFLGYITSAPGSRDYLQLTEHGNVKDIDSTDH
                                                                                                                                                                                                                                                                                                                                                                                                   63; Conserv
          Fungi;
                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Matches 116
                                                                     P95556;
P95556;
01-MAY-1997
01-MAY-1997
01-DEC-2001
ORF396 PROTE
Pseudomonas.
NCBI_TaxID=316;
[1]
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Lang F.B.F.;
Submitted (JUL-2001) to the EME
EMBL; AF402142; AAK83434.1; -.
Oxidoreductase; Mitochondrion.
OXIdoreductase; Mitochondrion.
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Forget L., Ustinova J., Wang Z., Huss V.A.R., Lan
"Hyaloraphidium curvatum: a linear mitochondrial
and an evolutionary link to lower fungi.";
                                    Pseudomonas
Bacteria; P
                                                             ORF396.
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SEQUENCE FROM
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                                     Proteobacteria;
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01-DEC-2001
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MEDLINE-99083431; PubMed-9866199;
Cao Y., Waddell P.J., Okada N., Hasegawa
"The complete mitochondrial DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Timkovich R., Zumft W.G.; "Resolution of the nirD locus for heme dl synthesis of cytochrome (respiratory nitrite reductase) from Pseudomonas stutzeri."; Eur. J. Biochem. 232:737-746(1995).
EMBL; Z73914; CAA98157.1;
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MEDLINE=96028114; PubMed=7588711;
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STRAIN-ZOBELL ATCC 14405;
                                                                            TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                     NADH5
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                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                 NCBI_TaxID=79736;
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1 (TrEMBLrel. 19, 1
ROGENASE SUBUNIT 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 396 AA; 43083 MW; EB07255ECFB1E0D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.5%;
21.1%;
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                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 128.5;
Pred. No. 0.
                                                                                                                                                                                                  Craniata; Vertebrata; Chondrichthyes; Galeoidea; Carcharhiniformes; Triakid
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        346
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  of.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147;
     the
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     shark (Mustelus
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                                                                                                                                                                                                    Triakidae;
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RESULT 10
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InterPro; IPR001516; Oxidored_q1_N.
InterPro; IPR000215; Serpin.
Pfam; PF00361; oxidored_q1; 1.
Pfam; PF00662; oxidored_q1_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB015962; BAA33045.1; -. InterPro; IPR003916; NADHub_oxdrdctse5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             manazo): Evaluating rooting contradictions
vertebrates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO1434; NADHDHGNASE5.
PROSITE; PS00284; SERPIN; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MO1. Biol. Evol. 15:1637-1646(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     155 VILTLSAIATLDRIGTDGDCSKPEEKKTGEVATGMASRPNW--LLAGAA-----FGSLV-
                                                    573
                                                                                                                                                     477
                                                                                                                                                                              547
                                                                                                                                                                                                       425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVIYNRIGDVGLILSMAWLATNLNSWEIHQLFILSKNKDLTLPLLGLVLAAAGKSAQFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPDPNPFGGAVLLCLASGLMLPSC-----LWFRGTGLI------WWVT-----GTASAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IILTLPLISSL-----SPKELK-----PNWSSLYVKTAVKISFFISLIP
                                                                                                                                                                                                      YSLRLIFFALMNYPRENTLSPINENNPLVINPIKRLAYGSIIAGLIITLNLT--
                                                                                                                                                                                                                                                                                                                               KSEKYMKLFLWLLVGVGLLGLGLRHKAYE----RKLG---KVAPTKEVSAAIWPFRFGYD
                                                                                                                                                                                                                                                                                                                                                         F----TASMWPQTLGHLINSGTNPGKTMTIAMIFYLLEIF-------FCAWCTAFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLLY------AAAVSGCVFAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DPNMNRFFKYLLFLISMIILVTANNMFQLFIGWEGVGIMSFLLIGWWYSRADANTAALQ
                                                 QQTSLIKLSTQPQQGLIK
                                                                          HREVSEKIHFNPRFGSYK
                                                                                                                           DHDRWCEYIMYRGLIR-LGY-ARISHAELSDSEIQMAKF---RIPDDPTNYRDNQKVVID
                                                                                                                                                                             THEGNHEDDLDRKLQATAVSKLLKSSSNQVIFLGYITSAPGSRDYLQLTEHGNVKDIDST
                                                                                                                                                                                                                             HTWGIM--ALSRYP-----IVKSEHHLLPSP-----EGEIAPAITLTVNISGKLVDFVV
                                                                                                                                                                                                                                                                             NEGWSSLERSAHLLNETGADFIT-ILESDASKPYMGNNDLTMWLGEKLGFYTDFGPSTRY
                                                                                                                                                                                                                                                                                                        CTHAFFKAMLFLCSG-----SIIHSLNDEQDIRKMGGLHKLLPFTSTSLTIGS-----
                                                                                                                                                                                                                                                                                                                                                                                                         HPWLPSAMEGPTPVSALLHS-----STMVVAGIFLLIRLHPLIQDNKLILTVCLCLGALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LFIFLDQGLESIVTNWNWMNMGPFDINMSFKFDLYSIIFTPVALYVTWSILEFALWYMHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------FLTHW-----SGHPHP
                                                                                                   SHFKTNPTLHYHHFSNLLGYFPSIIHRLLPKTSLNWAQYISTHLIDQTWNEKIGPKSNLI
                                                                                                                                                     -----PTKTQIMTMSPLLKLSALLVTIMGLLLA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                609 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                      -----LALTGMPFLSGFFSKDAIIESMNTSHLNAWALILTLVATSF---TAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68215 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oxidoreductase; Ubiquinone. 68215 MW; 97FBE6D34CDE7DD0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.3%;
19.3%;
                                                    590
                                                                            679
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3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No. 0.74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 8;
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AC AC

Q91VY8; Q91VY8;

PRELIMINARY;

PRT;

269 AA

Created)
 Last sequence update)
 Last annotation update)

Q

g

В

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RESULT 11
Q9GX6
ID Q9GX6; PRELIMINARY;
Q9GX6; PRELIMINARY;
Q9GX6; PRELIMINARY;
Q9GX6; PRELIMINARY;
Q9GX6; PRELIMINARY;
Q9GX6; PREMBLECT 16, C1
DT 01-MAR-2001 (TEMBLECT 16, L4
DT 01-UN-2001 (TEMBLECT 17, L4
DE SODIUM IODIDE SYMPORTER.
                         Query Natch
Best Local Similarity
Watches 71; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ery Match
st Local Similarity
                                                                                                                                                                                                                 TISSUE-THYROID;
Selmi-Ruby S., Rousset B.;
"Cloning of the pig sodium iodide symporter: Multiple isoforms generated by alternative splicing.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ276292; CAC17816.1; -.
InterPro; IPR001734; Na_solut_symport.
                                                                                                                                   PROSITE; PS00456; NA_SOLUT_SYMP_1; UNKNOWN_1.
PROSITE; PS50283; NA_SOLUT_SYMP_3; 1.
SEQUENCE 636 AA; 67165 MW; F80BBFD05152668F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases EMBL BC007125; AAH07125.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE-BREAST TUMOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197' LA------GAAFGSLV----FLTHWVFGEVSLVSRWAVSGHPHPGPDPNPF-GGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 WSGSHLQRYLRIWGFILGQIVLVVLRIWY-----TSLNPIWSYQMSNK----- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 AVLIYDFILAPRSSDFTDRMKVW 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 LLCLASGLMLPSCLWFRGTGLIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 LAHGVNSGQGLGIEIIGTLQLVLCVLATTDRRRRDLGGSAP-----LAIGLSVALGHL 181
15 GCVSWSLYHDLGPMI-----YYFPLQTL----ELTGLEGFSIAFLSPIFLTITPFWK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 FWKLVNKKWM-LTLLRIITIGSIASFQAPNAKLRLMV------LALGVSSSLIVQAVTW 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAIDYTGCSINPARSFGSAVLTRNFSNHWIF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FWRAVVAEFLAMTLFVFISIGSALGFNYPLERNQTLVQDNVKVSLAFGLSIATLAQSVGH 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISGAHLNPAVTL-GLLLSCQISILRAVMYIIAQCVGAIVATAILSGITSSLVDNSLGRND 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *------VILTLSAIATLDRIGTDGDCSKPEEKKTGEVATGMASRPNWL 196
                                                                                                                                                                                                      PF00474; SSF;
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                  3.3%;
                                              43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                           Score 122; DB 6;
Pred. No. 1.1;
3; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 123.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80534DE4B78AB5E7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 11;
                                                103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -WV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82;
                                                                                       Length 636;
                                              Indels 100;
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                                              Gaps
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DЬ Q

472

SMG---VLPSSA---

150

QMSNKVILTLSAIATLDRIGTDGDCSKPEEKKTG------

DЬ Ş

519 AASFYAISYLYYGALGTLSTI----

199 GAAFGSLVFLTHWVFGEVSLVSRWAVSGHPHPGPDPNPFGGAVLLCLASGLMLPSCLWFR 258

---LCGALISCL-TGPTKRSAL---

557

-----AGCALPTANASGLQDPVLAVNASSTASSLETDPEQPIL 518

-EVATGMASRPNWLLA 198

Db δÃ В Ş

Be Ma

В Q

	63 LVNKKWNLTLLRIITIGSIASFQAPN-AKLRLMVLALGVSSSLIVQAV-TWWSGS 115	
	15 GCVSWSLYHDLGPMIYYFPLQTLELTGLEGFSIAFLSPIFLTITPFWK 62 :: :: :: : : 300 GIVMFALYVDCDPLLAGHISAPDQYMPLLVLDIFEDLPGVPGFLACAYSGT 351	
16;	ery Match 3.3%; Score 122; DB 6; Length 643; st Local Similarity 22.4%; Pred. No. 1.1; caps 103; Indels 100; Gaps	CT 00 (D
	PROSITE; PS00456; NA_SOLUT_SYMP_1; UNKNOWN_1. PROSITE; PS50283; NA_SOLUT_SYMP_3; 1. SEQUENCE 643 AA; 68127 MW; 29B111986C8E8443 CRC64;	
	NCE FROM N.A. E=THYROID; -Ruby S., Rous; ing of porcine tted (MAR-2000 AJ276242; CAC AJ276242; CAC PRO01734	
	2001 2001 10DI	
	LT 12 X7 X7 X7 AGGIX7 PRELIMINARY; PRT; 643 AA.	~ ~ ~
	259 GTGLIWWVTGTASAA 273 	
	199 GAAFGSLVFLTHWVFGEVSLVSRWAVSGHPHPGPDPNPFGGAVLLCLASGLMLPSCLWFR 258 : :: : : : : : : : : :	
	150 QMSNKVILTLSAIATLDRIGTDGDCSKPEEKKTGEVATGMASRPNWLLA 198	
	116 HLQRYLRIWGFILGQIVLVVLRIWYTSLNPIWSY 149	
	63 LVNKKWMLTLLRIITIGSIASFQAPN-AKLRLMVLALGVSSLIVQAV-TWWSGS 115	

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Best Local
                                     Q36149;
Q36149;
01-NOV-1996
01-NOV-1996
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "pyrococcus abyssi genome sequence: insights i structure and evolution.";
Submitted (JUL-199) to the EMBL/GenBank/DDBJ EMBL; AJ248287; CAB50367.1; -
InterPro; IPR003674; OTase_STT3.
Pfam; PF02516; STT3; 1.
Complete proteome.
SEQUENCE 766 AA; 87894 MW; C7A7E52701819CE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TremBLrel. 13, Created)
01-MAY-2000 (TremBLrel. 13, Last sequence update)
01-JUN-2001 (TremBLrel. 17, Last annotation update)
TRANSMEMBRANE OLIGOSACCHARYL TRANSFERASE, PUTATIVE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9UYP5;
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Trachemys
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                           NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT
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                                                                                                                                                                                                                                                                                                                                                                                                                      LLVGVGLLGLGLRHKAYERKLGKVAPT - · KEVSAAIWP - - - - - FRFGYDNE - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----VIFGTLTIVFFYISLLKLYGKEKAFFASIFLALSFGHIFRSMANYYRGDNYMLFW
                                                                                                                                                                  WKAFSISIFLLPLFFLRF-HPEKVKTE
                                                                                                                                                                                          WCEYIMYRGLIRLGYARISHAELSDSE
                                                                                                                                                                                                                      FLSRFVKSKRAKVGIVIGLGTVSILIILLKFPALRGLLGIFDMFKSTPIMETRPTNFHDL
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                                                                                                                                                                                                                                                                                                                                     LDKKRNFLD----SFIIIL-STAFGAIIAN----YLGEKFGY-------
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scripta (Red-eared slider turtle) (Pseudemys scripta).
                                       (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence up)
(TrEMBLrel. 19, Last annotation)
                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                              3.3%; Score 122; DB 17;
23.5%; Pred. No. 1.4;
tive 53; Mismatches 153;
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yar mitochondrial genes for NADH-ubiquinone oxidoreductase subunit 5.

"Ar cytochrome coxidase subunit 1.",
"AL BIOCHEM. 241:83-92(1996).
"C :- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.

EMBL; U49048; AAC60055.1; -.

"R EMBL; U49048; AAC60055.1; -.

"R InterPro; IPR001916; NADHHb oxdrdctse5.

"InterPro; IPR001916; Oxidored_q1."
"InterPro; IPR001916; Oxidored_q1."
"InterPro; IPR001916; Oxidored_q1."
"InterPro; IPR001412; tRNA-synt_I.
"R Ffam; PF00361; oxidored_q1; 1.
"P Ffam; PF00362; oxidored_q1; 1.
"P Ffam; PF00662; oxidored_q1, 1.
"P Ffam; PF001434; MADHHGHANSE5.
"P RROSITE; PS00178; AA_TRNA_LIGASE_I; UNKNOWN_1.

Mitochondrion; NAD; Oxidoreductase; Ubiquinone.

SEQUENCE 591 AA; 68062 MW; 1C577C2B77EF901A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Testudines; Cryptodira; Testudinoidea; Emydidae; Trachemys. NCBI_TaxID=34903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97054595; PubMed=8898892;
Cai Q., Storey K.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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TMTMPMWIKIAALTVTVIGLLVGL--
                                                                                                                                                                                                                         NMLFGPKKNLDLLLQTKNSSKVLFRKSEKYMKLFLWLLVGVGLLGLGLRHKAYERKLGKV
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                                                              YTLRIMLLVQTGHPLQNSTYLLHENIPTIMNPITRLATGSIMA---GWLITKNIQMFNTP
                                                                                              YMGNNDLTMWLGEKL-----
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                            EGETAPAI - - - TLTVNISGKLVDFVVTHFGNHEDDLDRKLQATAVSKLLK - - - - SSSNQV
                                                                                                                            HKPLPITSACLTIGNMALMGMPFLTGYYSKDAIIETMSTSYLNSC-ALLLTLMATSFTAV
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                                                                                                                                                           -WPFRFGYDNEGWSSLERSAHLLNETGADFITILESDASKP
                                                                                                                                                                                           -LHICMHAFFKAMLFMCAGFIIHSLG--NEQDIRKMGGL
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Pred. No. 1.
                                                                                          -GFYTDFGPSTRYHTWGIMALSRYPIVKSEHHLLPSP
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KVVCMATKKPLKPYKTCDPTSM
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01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001516; Oxidored_ql_N.
Pfam; PF00361; Oxidored_ql_; 1.
Pfam; PF00662; Oxidored_ql_N; 1.
PRINTS; PR01434; NADHDHGNASE5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ratite evolution.";
Nature 409:704-707(2001).
-I- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Palaeognathae; Casuariiformes; Casuariidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 605 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDLINE-21085666; PubMed-11217857;
Coper A., Lalueza-Fox C., Anderson S., Rambaut A., Austin J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CBI_TaxID-30463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           618
                                            246 ALLHS----STMVVAGIFLLIRTHPLLTNNQTALTTCLCLGALSTLFAATCALTQNDIK
                                                                                        304 HLINSGTNPGKTMTIAMIFYLLE-----IFFCAWCTAFKFVPGGVYARERSDV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nterPro; IPR001750; Oxidored_q1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete mitochondrial genome sequences of two extinct moas clarify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       503 AGLSQLPSPPQYIKKYLKMAQKIATHLADTS----WFEYLGPKVTAKWQKTPMRFTSLMQ 558
                                                                                                                                                                                                                                                                   185 VATGMASRPNWLLAGAAFGSLVFLTHWVFGEVSLVSRWAVSGHPHPGPDPNPFGGAVLLC 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               suarius
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Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 RGLIRL 623
: |||::
9 KGLIKI 564
                                                                                                                                                                                LASGLMLPSCLWFRGTGLIWWVTGTASAAGLLYLHTW-AAAVSGCVFAIFTASMWPQTLG 303
                                                                                                                                                                                                                                                                                                               NNMFMLFIGWEGVGIMSFLLIGWWHGRAEANTAALQAV-IYNRIGDVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PMIYYEPLOTLELTGLEGESI-----AFLSPIFLTITPFWKLVNKKWMLTLLRIITIG 79
                                                                                                                                    ----MLPL-----LGLILAATGKSAQFG---LHPWLPAAMEG-----
                                                                                                                                                                                                                                                                                                                                                           ----LRIWYTSLNPI-----WSYQMSNKVILTLSAIATLDRIGTDGDCSKPEEKKTGE 184
                                                                                                                                                                                                                                                                                                                                                                                                     +-LSFKMDQYSMLFFPIALFVTWS-ILQFATWYMASEPHITKFFIYLLTFLIAMLTLTIA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIASFQAPNAKLRLMVLALGVSSSLIVQAVTWWSGS--HLQR-YLRIWGFILGQIVLVV- 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PMSITSTVKTAFFTSLIPMSIFIYSGTETIVSQWYWNFTPNFKIP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IFLGYITSAPG-SRDYLQLTEHGNVKDIDSTDHDRWCEY--
-----LLGTMMLIIGLNMLFGPKKNLDLLLQTKNSSKVLFRKSEKYMKLFLWLLVG 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AY016011; AAK08552.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                         -------LILSMAWL---ASTINTWEIQQASYETQMP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oxidoreductase; Ubiquinone. 66408 MW; 41B286D9EC828A26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.3%; Score 121; DB 8; Length 605; 19.6%; Pred. No. 1.2; tive 87; Mismatches 230; Indels 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oxdrdctse5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    605 AA
                                                                                                                                    ----PTPVS 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMY 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                              300
                                                                                        351
                                                                                                                                                                                                                            210
                                                                                                                                                                                                                                                                                                                    183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34;
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	546 GQKIASHLIDLSWYKKMGPEGLADLQLMAAKTSTP 580	Db 5
LG-YARISHAELSDSEIQMAK	598 GNVKDIDSTDHDRWCEYIMYRGLIRLG-YARISHAELSDSEIQMAKFRIP	0у 5
NLTPSKQNTYSNFSITLGYFN	491 AIIVTILGIMLALELLNLTHNLTPSKQNTYSNFSITLGYFNPLLHRLNPMMLLNN	Db 4
LLKSSSNQVIFLGYIT	543 DFVVTHFGNHEDDLDRKLQAIAVSKLLKSSSNQVIFLGYITSAPGSRDYLQLTEH	Qy 5
TRLAVGSI IAGLLITSNVLPT	439 PPITPINENSPAVTNPITRLAVGSIIAGLLITSNVLPTKTPPMTMPMVTKMA 490	Db 4
	511 PIVKSEHHLLPSPEGEIAPAIT	Qy 5
SIRMTLMVQAGE	404YLN-TWALLLTLLATSETATYSIRMTLMVQAGETRI 438	Db 4
NNDLTMWLGEKLGFYTDFGPS	451 AHLLNETGADETTILESDASKPYMGNNDLTMWLGEKLGEYTDEGPSTRYHTWGIMALSRY 510	0у 4
TTTACLTIGSLALMGTPFLAG	346 SIIHSLGGEQDIRKMGGLQKLLPTTTACLTIGSLALMGTPFLAGFYSKDLIIESLNNS 403	Db 3
TKEVSAAIWPFRFO	403 VGLLGLGLRHKAYERKLGKVAPTKEVSAAIWPERFGYDNEGWSSLERS	Оу 4
 PQLAFLHIS	301 KIIAFSTSSQLGLMMVTIGLNL	Db 3

Search completed: October 21, 2002, 22:10:57 Job time: 68 secs